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Result
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Listing first 45 s
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Copyright (c) 1993 - 2000 Comp
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S. lavendulae Mit
S. lavendulae Mit
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159.5	160	162.5	162.5	162.5	164.5	165	168	168.5	169.5	170	170	172	173.5	177	177	178	178	179	182	182	182	185	185	185	185	187	187	187	187	187	187	188	188	
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357	361	581	366	344	350	349	275	266	114	383	352	115	266	348	308	348	348	280	348	344	308	318	318	318	301	365	358	336	336	293	293	366	361	
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AAY34114	AAW70837	AAG31804	AAY96473	AAW70838	AAY96472	AAY96462	AAY39302	AAG51383	AAB32486	AAW70836	AAY96469	AAB32490	AAG07858	AAG51381	AAG51382	AAY77937	AAW95017	AAW17977	AAG07856	AAY80992	AAG07857	AAB46832	AAB46831	AAY69405	AAB46833	AAG45953	AAG45950	AAG45954	AAG45951	AAG45955	AAG45952	AAG21650	AAG21524	
Maize cyclopropane	Arabidopsis SMT en	Arabidopsis thalia	Soybean gamma-toco	Corn SMT enzyme.	Soybean gamma-toco	Soybean gamma toco	SpnF protein invol	Arabidopsis thalia	SAM dependent meth	Yeast SMT enzyme.	Corn gamma-tocophe	SAM dependent meth	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis gamma-	S-adenosyl methion	Arabidopsis thalia	Maize C-24 sterol	Arabidopsis thalia	Synechocystis PCC6	Synechocystis PCC6	Amino acid sequenc	Synechocystis PCC6	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia					

ALIGNMENTS

AAB80627 RESULT WPI; 2001-147355/15. N-PSDB; AAF74206. Yamada A, 19-JUL-1999; 99JP-0235910. 24-MAR-2000; 2000JP-0085377. 19-JUL-2000; 2000WO-JP04862 25-JAN-2001. WO200106006-A1 Sueada japonica. Environmental stress resistance; salt; heat; desert; transgenic plant. Environmental stress tolerant protein SEQ ID 40 02-MAY-2001 AAB80627; AAB80627 standard; Protein; (NISC-) JAPAN SCI & TECHNOLOGY CORP. Ozeki Y, (first entry) Saito T; 473 AA

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dimethylglycine content; abiotic stress; to
cold; drought stress; pathogenesis-related
                                                            A. halophila sarcosine-dimethylglycine methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA from a library originating in a salt-resistant organism into a cell, culturing the transformants under conditions in which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences AAF74187 - AAF74218 encode proteins AAB80608 - AAB80639, which impart environmental stress resistance. The invention relates to a method for identifying DNA encoding proteins imparting environmental stress resistance. The method comprises inserting
                                Sarcosine-dimethylglycine methyltransferase; SDMT; betaine operon;
                                                                                              05-JUN-2000
                                                                                                                                                          AAY70038 standard;
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yelsllsckcigayvrnkknqnqişwlwqkvdskddkgfqrfldtsqykcnsilryervf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention.
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                                                                                              (first
                                                                                                                                                          protein;
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86.4%; Pred. No. 3
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3.9e~198;
hes 30;
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 protein;
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 salt; freezi
animal feed;
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Matches 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New methyltransferases, useful for e.g. producing transgenic plants with increased stress tolerance, pathogen resistance or nutritional value as animal feed or for improving the viability of microorganisms in the food industry
                                21-MAY-1999
                                                               AAW95016;
                                                                                              AAW95016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterologous protein
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                             (first entry)
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26.3%; Pred. No. 4.5e-11;
tive 44; Mismatches 120
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Synechocystis gamma-tocopherol methyltransferase (gamma-TMT).

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respectively. The DNA fragments are useful for producing transgenic plants containing a higher alpha-tocopherol; gamma-tocopherol ratio. They are also useful for producing alpha-tocopherol and plants with increased gamma-tocopherol, which may be useful in certain industries such as the meat industry e.g. for developing forage plants to feed animals. The production of transgenic plants (and seeds) with a higher alpha-tocopherol ratio, using the gamma-TMTs, will increase the level of alpha-tocopherol ratio, using the gamma-TMTs, will increased the stability and shelf life of plants and plant products. Increased levels of alpha-tocopherol will also increase meat quality and extend shelf life of post-processed meat products. Plants with a higher alpha-tocopherol ratio may also produce advantageous phenotypes. The present sequence represents a Synechocystis gamma-TMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
25-JUL-1997;
26-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides DNA sequences encoding gamma-tocopherol methyltransferases (gamma-TMT). The gamma-TMT encoding genes SLR0089 and 165H5T are isolated from Synechocystis and Arabidopsis species and the state of the state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newly isolated DNA fragment comprising a ^c-tocopherol (vitamin E) methyltransferase coding sequence - useful for producing ^a-tocopherol, and transgenic plants, seeds and oils with an altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gamma-tocopherol methyltransferase; gamma-TMT; SLR0089; 165H5T7; meat;
transgenic plant; alpha-tocopherol; gamma-tocopherol; forage plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYNE-) UNIV
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                                                               389
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                                                                                                                                                                                         329
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      200
                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 7.9%; Score 204.5; DB 20; Local Similarity 26.3%; Pred. No. 8.2e-11; les 61; Conservative 48; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                         YVKSKKNQNQISWLWQKVDSEDDKGFQRFLDSSQYKFNSILRYERVFGPGYVSTGGLETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-142458/12.
DB; AAX17788.
                                                               YC-
                                                                                                                                                                                   IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISD
                                                                                                                                                                                                                                                                                                         KEF----VSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALE--RS 328
                                                                                                                                                                                                                                                                                                                                                                  yekiknfyddssglwedvwge----hmhhgyygphgtyridr
                                                                                                                         lglgstcqfqvanaldlpfasdsfdwvwslesgehmpnkaqflqeawrvlkpggrlilat
wchrpidpgngpltaderrhl-qaiydvyclpyvvslpdyeaiarecgfgei
                                                                                                                                                                                                                                               kellawavpqnsakp-rkildlgcgiggsslylaqqhqaevmgaslspvqveragerara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 33-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
                                                         --KSAGTPSAEFAAYIRQRGYDLH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEVADA
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97US-0053819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46pp; English
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                                                            --DVKAYGKMLKDAGFVEV 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT AAY39308

Best Local Similarity 25.7 Matches 53; Conservative

7.6%; Score 198; DB 20; 25.7%; Pred. No. 2.8e-10; tive 44; Mismatches 97

97;

12;

Gaps

5

Length 283; Indels

Sequence

ΑA;

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cc macrolide producers. The spinosyn PKS DNA region consists of 5 ORFs with Cs stop codons at the end of acyl carrier protein (ACP) domains. Together the PKS polypeptides (AAY39297-Y39301), form a complex consisting of an initiator module, spnA, and several extender modules spnB-spnE. The products of the genes present in the region upstream of the PKS genes can be assigned names spnF-spnS AAY39302-Y39315 and are responsible for different modifications in spinosyn biosynthesis. There are also two CC ORPs ORF115 and ORF116 present immediately upstream of spnS, producing colypeptides AAY39316-Y39317, and two ORFs ORF1 and ORF2 present cc downstream of the PKS region producing polypeptides AAY39316-Y39317, and two ORFs ORF1 and ORF2 present cc is suggested that SpnL is involved in C-methylation during spinosyn complication new spinosyns e.g. by mutagenesis, or interruption of steps constrol agent or serve as substrates for further chemical modification cand the creation of new semi-synthetic spinosyns. The genes are also useful to isolate similar sequences from S. spinosa or other species by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltz RH,
Treadway H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microlides; arachnid; nematode; insect; polyketide; polyketide synt) PKS; extender module; initiator module; acyl transferase domain; AT, acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; enov1 reduction 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the product of the spnL gene. The protein is involved in spinosyn biosynthesis. The SpnL gene is one of 23 genes and open reading frames contained in an 80kb DNA sequence AAZ21501. Spinosyns are insecticidal microlides which are useful for the control of arachnids, nematodes and insects. Biosynthesis of spinosyns occurs via stepwise condensation and modification of carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY39308 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursors generating a linear polyketide which is modified further. To DNA sequence contains a central region of approximately 55kb which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 156-157; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOWC ) DOW AGROSCIENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SpnL protein involved in spinosyn biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology to the DNA encoding the polyketide synthases (PKS) of known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spinosyn biosynthétic genes from Saccharopolyspora spinosa, useful production of insecticidal spinosyn compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ľď,
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J, Turner JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-methylation.
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Waldron C
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В

Query Match

DB 21;

Length

279;

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RESULT
AAY70041
                            result of abiotic stress, and the polynucleotide can be used to increase salt, freezing or cold tolerance, increase resistance to drought stress, pathogens or induce pathogenesis-related proteins in plants. Transgenic organisms can be used as an animal feed ingredient. The polynucleotide can also be used to enhance pH tolerance and improve viability of organisms when subjected to environmental stress. This can decrease inclusion body formation when used in conjunction with polynucleotides
                                                                                                                                                                                                                                       The present sequence is Ectothiorhodospira halochloris sarcosine dimethylglycine methyltransferase (SDMT) catalysing conversion of sarcosine to dimethylglycine. Expression vectors comprising the coding region from betaine operon can be used to increase intracellular betaine and dimethylglycine content. Betaine is accumulated in the cells as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New methyltransferases, useful for e.g. producing transgenic plants with increased stress tolerance, pathogen resistance or nutritional value as animal feed or for improving the viability of microorganism in the food industry .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sarcosine-dimethylglycine methyltransferase; SDMT; betaine opero dimethylglycine content; abiotic stress; tolerance; salt; freezi cold; drought stress; pathogenesis related protein; animal feed; pH tolerance; environmental stress; inclusion body formation.
encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 163-164; 176pp; English
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   heterologous
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   protein.
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Sequence

279

This invention relates to isolated and purified nucleic acid molecules from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae

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AAB32508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                Novel nucleic acid molecule comprising mitomycin biosynthetic cluster useful for cloning mitomycin biosynthetic genes for eithe molecular basis of mitosane ring system biosynthesis -
                                                                                                                                                         Sherman
                                                                                                                                                                                                  (MAOY/)
(VARO/)
                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory; immune-enhancer; immunosuppressant; chronic obstructive pulmonary disease; respiratory inf
                                                                                                                                                                                                                                                                                                                                                                                        Mitomycin;
                                                             Disclosure;
                                                                                                                                                                                                                                                                        10-MAR-2000; 2000WO-US06394.
                                                                                                                                                                                                                                                                                                                                      Streptomyces lavendulae.
                                                                                                                                                                                                                                                                                                                                                                                                              S. lavendulae Mit N encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB32508
                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                             14-SEP-2000.
                                                                                                                                                                                                                                                                                                                  WO200053737-A2
                                                                                                                                                                                                                                                                                                                                                         fungicide;
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                                                                                                                                                                              (SHEL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 TKEFVSKL--DLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERSIGL 331
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DB; AAC55801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tvermsslsrqlgpdsyvldmgagyggsarylahkygckvaalnlser--enerdrqmnk 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                         DH,
                                                                                                                                                                             HE M.
SHELDON P
                                                                                                                                                                                                           SHERMAN D H.
                                                                                                                                                                                                                                 UNIV MINNESOTA.
                                                                                                                                                                                                 VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                         pesticide
                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; mitosane ring system; antibiotic; anti-cancer;
                                                            Page 354; 399pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                        Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                    99US-0266965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YCKSAGTPSAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.48;
                                                                                                                                                         Varoglu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence
                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275
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Pred. No. 7.3e-10;
Pred. No. 7.3e-10;
                                                                                                                                                         He
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                                                                                                                                                         Sheldon
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elucidating
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RESULT
AAB32507
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Best Local
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                              (MINU)
(SHER/)
(MAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer; anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. lavendulae Mit M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB32507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning of the mitomycin biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibiotics, anti-inflammatory agents, anti-cancer agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                             12-MAR-1999;
                                                                                                                                                                                                                         10-MAR-2000;
                                                                                                                                                                                                                                                                                         14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                        WO200053737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungicide; pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences and the transformed
(VARO/)
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                              ) UNIV MINNESOTA.
) SHERMAN D H.
) MAO Y.
VAROGLU M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275
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                                                                                                                                                                                                                         2000WO-US06394.
                                                                                                                                                             9905-0266965
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Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          host cells of the invention result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes.
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immune-enhancers, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer PHA monomer synthases. Sequences AACS5782-C55881, AAC55815-C55849 and AAB32485-B32542 represent mitomycin biosynthetic gene cluster DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEMM/)
                                     cloning of
                                                              sequences and encoded proteins. Sequences AAC55812-C55814, AAC55850-C55856 and AAC55862-C55869 represent PCR primers used in the
                                                                                                                                                                                                                                                                                                            antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well
                                                                                                                                                                                                                                                                                                                                                                              spanning 55kb of DNA. The invention includes an expression casset comprising a mitomycin biosynthetic gene operably linked to a pro and host cells transformed with the cassette. The nucleotide and sequences and the transformed host cells of the invention result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae mitomycin biosynthetic gene cluster comprises 47 mitomycin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 353; 399pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis \,\cdot\,
Sequence
                                                                                                                                                                                                                                                                antibiotics, anti-inflammatory agents, anti-cancer agents,
                                                                                                                                                                                                                                                                                       as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-601980/57
DB; AAC55802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to isolated and purified nucleic acid molecules
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SHELDON P C
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                                                                       AAG21652 standard; Protein;
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                                                                                                                                                              rllserinsskqrle---tqfgeemvnqfdpg---dlv--
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Arabidopsis thaliana protein

fragment

SEQ ID

NO: 24284.

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	Protein identification; hybridisation assay; ge termination sequence. Arabidopsis thaliana.
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	transduction pathway; pping; gene expression
	metabolic control;
	<pre>pathway; promoter;</pre>
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RESULT
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36; Mismatches 93;
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9908-0161359
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27.3%;
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                                                                                                                                   Score 188; DB
Pred. No. 3.2e
36; Mismatches
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3.2e-09;
nes 93;
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990S-0138647
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99US-0123180.
99US-0123548.
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Protein identification; signal transduction hybridisation assay; genetic mapping; gene e termination sequence.
                                                                                                                           Arabidopsis thaliana protein fragment
Arabidopsis thaliana.
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                                                                                                                                                                                                                                                        standard; Protein;
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                                                                                                                           SEQ ID NO:
                                                             n pathway; metabolic
expression control;
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                                                             pathway;
promoter;
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18-AUG-1999
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29-SEP-1999
21-CCT-1999
22-CCT-1999
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{\tt vkadfmkmpfpensfdavyaieatchapdaygcykeiyrvlkpgqcfaayewcmtdafdplayedfabeta}
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                                                                             ch 7.2%;
l similarity 27.3%;
65; Conservative
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990S-0149722
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990S-0161359
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; Pred. No. 3.2e-09;
36; Mismatches 93;
                                                                                               Length
                                                                               Indels
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                      396
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18-JUN 1999
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990S-0136392. 990S-0136782. 990S-013722. 990S-0137528. 990S-0137524. 990S-0138540.	990S-0132487. 990S-0132863. 990S-0134256. 990S-0134218. 990S-013421. 990S-013421. 990S-0134768. 990S-0134768. 990S-0134768. 990S-0134768. 990S-0134768. 990S-0135629.	990S-012462. 990S-0128234. 990S-0128234. 990S-0128714. 990S-0130445. 990S-0130077. 990S-0130449. 990S-0130481. 990S-0130481. 990S-0132488. 990S-0132488.	thaliana. 2000EP-0301439. 2000EP-031180. 99US-012180. 99US-012548. 99US-012564. 99US-0125788. 99US-0125788.	standard; Protein; 361 AA. ; ; ; ; ; ; ; ; ; ; ; ; ;	SAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEVIAENR
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9US-014730 9US-014730 9US-014719 9US-014726 9US-014730 9US-014741 9US-014741	903-0145192 903-0145145 903-0145214 903-0145214 903-0145213 903-0145213 903-0145913 903-0145913 903-0145318 903-0145318	9US-01443 9US-01443 9US-01443 9US-01443 9US-01443 9US-01448 9US-01448 9US-01448 9US-01450 9US-01450	9US-0141287 9US-01421842 9US-0142055 9US-0142055 9US-0142390 9US-0142803 9US-0142803 9US-0142977 9US-0143542 9US-0143624	99US-0139458 99US-0139469 99US-0139461 99US-0139462 99US-0139763 99US-0139750 99US-0139763 99US-013989 99US-0140353 99US-0140354 99US-0140823 99US-0140991	9US-01388 9US-01391 9US-01394 9US-01394 9US-01394 9US-01394 9US-01394 9US-01394

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17-AUG-1999;
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14-OCT-1999;
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280 KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEF 337
                            th 7.2%;
Similarity 27.3%;
65; Conservative
                                                             990S-0148171
990S-0148149
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990S-0161161
                             36;
                            Score 188; DB 21;
Pred. No. 3.5e-09;
6; Mismatches 93;
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                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0129845.
990S-0130049.
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05-AUG-	04 - AUG - 04 - AUG -	02-AUG-1999; 03-AUG-1999;	02-AUG-	28-JUL-	27 - JUL -	27-JUL-	23 - JUL -	23-JUL-	23-JUL-	22-JUL-	22-JUL-	22-JUL-	21 - JUL -	21-JUL-	20-JUL-	20-JUL-	20-JUL-	19-JUL-	19-JUL-	19-JUL-	19-JUL-	16-JUL-	16-JUL-	15-JUL-	13-JUL- 14-JUL-	12-JUL-	-JUL-60	-TOF-80	06-JUL-	01-JUL-	01-JUL-	30-JIN-	28-JUN-	24 - JUN-	23 - JUN -	22-JUN-	18-JUN-	18-JUN-	18-JUN-	TB-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	17-JUN-	16-JUN-	14 - JUN-	10-JUN-	08-JUN-	07-JUN-	03-JUN-
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7	9908-016	99US-0161 99US-0161	99US-016	9908-016	99US-016	9908-016	99US-016	99US-016	9905-016	99US-016	99US-016	99US-016	9905-016	9908-015	99US-015	9905-015	9905-015	9905-015	99US-015	99US-015	9908-015	99US-015	99US-015	9905-015	9908-015	9905-015	99US-015	99US-015	9908-015	9908-015	9908-015	910-2166	9905-015	9905-015	9908-015	99US-015	9905-015	99US-015	9908-015	9908-014	99US-014	9908-014	9905-014	9905-014	99US-014	99US-014	9905-014	99US-014	99US-014	9905-014	99US-014	99US-014	99US-014
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09-MAR-1999
09-MAR-1999
23-MAR-1999
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01-APR-1999
01-APR-1999
16-APR-1999
21-APR-1999
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14-MAY-1999
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hybridisation assay; ger
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   9908-0123180

9908-0123788

9908-0126785

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9908-012871462

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9908-0130449

9908-0130891

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9908-0131449

9908-0132484

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netic mapping; gene expression control; promoter;
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27-MAY 1999
28-MAY 1999
28-MAY 1999
30-JUN 1999
30-JUN 1999
31-JUN 1999
32-JUN 1999
32-JUN
 990S-0135629
990S-0136782
990S-0136782
990S-0136782
990S-0137522
990S-0137522
990S-0138640
990S-0139451
990S-0139451
990S-0139452
990S-0139452
990S-0139452
990S-0139465
990S-0139465
990S-0139465
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  25-REB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

01-APR-1999

16-APR-1999

17-APR-1999

23-APR-1999

23-APR-1999

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23-APR-1999

23-APR-1999

23-APR-1999

14-MAY-1999

06-MAY-1999

07-MAY-1999

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01-MAY-1999
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28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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990S-0121825
990S-0123180
990S-0125788
990S-0125788
990S-0126785
990S-0127462
990S-0128714
990S-0129845
990S-013049
990S-0131449
990S-0131449
990S-0132486
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99US-0161993.
99US-0162142.
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Pred. No. 3.2e-09;
6; Mismatches 93;
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napping; gene expression control; promoter;
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9908-0147260
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9908-01481715
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12-AUG-1999
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27-AUG-1999
27-AUG-1999
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31-AUG-1999

9-AUG-1999; 9-AUG-1999; 0-AUG-1999; 1-AUG-1999;

5-AUG-1999; 5-AUG-1999; 5-AUG-1999;

2-AUG-1999; 3-AUG-1999; 4-AUG-1999; 4-AUG-1999; 5-AUG-1999;

99US-0146389. 99US-0147038. 99US-0147204. 99US-0147302. 99US-0147192.

13-SEP-1999
15-SEP-1999
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20-SEP-1999
22-SEP-1999
23-SEP-1999
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26-SEP-1999
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7 - JUN - 1999 8 - JUN - 1999 9 - JU	14 - MAY - 1999; 18 - MAY - 1999; 19 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 03 - JUN - 1999; 03 - JUN - 1999;
990S-0137502 990S-0137702 990S-0138540 990S-0138547 990S-0139453 990S-0139453 990S-0139454 990S-0139456 990S-0139461 990S-0139461 990S-0139461 990S-0139461 990S-0139462 990S-013963 990S-0140695 990S-0140695 990S-014082 990S-014082 990S-014082 990S-014082 990S-014082 990S-014483 990S-0145085 990S-0145085 990S-0145183 990S-0145183 990S-0145183 990S-0145218	99US-0134370. 99US-0134768. 99US-0135941. 99US-0135353. 99US-0135629. 99US-0136021. 99US-0136782. 99US-0136782. 99US-0137528.
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28-OCT-1999;
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-455-543A-56

US-08-455-343A-53

US-08-223-305C-53

US-08-25-343A-52

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US-08-213-305C-55

US-08-233-305C-55

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ALIGNMENTS	US-08-785-396-4 US-08-938-291A-4	US-08-374-155A-4	US-08-785-396-10	US-08-374-155A-10	US-09-147-522-9	US-09-218-032-4	US-09-102-644-4	US-09-103-509-4	US-08-966-389-4	US-08-961-083-64	US-08-149-223A-10	US-08-458-731-10	US-08-480-150A-10	US-08-484-596A-10	US-08-484-158B-10	US-08-484-993B-10	US-08-223-305C-54
	Sequence 4, Appli Sequence 4, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 9, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 64, Appl	•	Sequence 10, Appl	Sequence 10, Appl	`	-	Sequence 10, Appl	Sequence 54, Appl

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RESULT 1
US-09-041-718-5
; Sequence 5, Application US/09041718A
; Sequence 5, Application US/09041718A
; Patent No. 6225075
; GENERAL INFORMATION:
; APPLICANT: Bard, Martin
; APPLICANT: Bard, Martin
; TITLE OF INVENTION: DNA encoding sterol methyltransferase
; FILE REFERENCE: 740.003US1
; TITLE OF INTORNAL NUMBER: IIS/09/041.718A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 5; LENTH: 363; TYPE: PRT; ORGANISM: Triticum atrivum US-09-041-718-5
                                                                                                                                                                              US-09-036-987A-13
                                                                                                                                                                                                     RESULT
                                                                                                                       Sequence 13, Application US/09036987A Patent No. 6143526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                     GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
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Baltz, Richard H.
Broughton, Mary C.
Crawford, Kathryn P.
Madduri, Krishnamurthy
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APPLICANT: Waldron, Clive TITLE OF INVENTION: Biosynthet TITLE OF INVENTION: Production

Biosynthetic Genes For Spinosyn Insecticide

Waldron,

Treadway, Patti J. Turner, Jan R.

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US-09-029-603-2

; Sequence 2, Application US/09029603

; Patent No. 6210935
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                                                                                                                                                                          GENERAL INFORMATION:
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Best Local :
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CURRENT APPLICATION NUMBER: US/
                                      APPLICANT: Toupet, Christine
APPLICANT: Posphech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
                                                                                                              APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Bietenhader, Jurg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30 APPLICATION DATA: APPLICATION NUMBER: U5/09/036,987A FILING DATE: 09-MAR-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  443
                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 GLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDY 389
                                                                                                                                                                                                                                                                                                              215 LRKLDELAGVEPAAVGTYQQRYLGDI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 ETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 9330 zions
CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
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REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                  QKELDALEQEKDDFIDDFSEEDYNDI
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                                                                                                                                                                                                                                                                                                                                                                                                                          CKSAGTPSAEFAAYIRQRGYDLHDVKAYGKMLKDAGF----VEVIAENR--TDQFIQVL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLAGSLEFDLVDGAQLPYPDGFFQAAWAMQSVVQIVDQAAAIREVHRILEPGGRFVLGDI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLTDLFIDKAALRPGAHLFDLGCGNGQPVVRAACASGVRVTGITVNAQHLAAATRLANET 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46268
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25.7%;
                    US/09/029,603
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Pred. No. 2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08457245 Patent No. 5573915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 280
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BARRY
APPLICANT: YUAN,
                                                                         TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptomyces longisporoflavus FEATURE:
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                             REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Guy W.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 TTADIDDYVALLHRSGLRLREI 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 GIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEFEVADCTKKDYPENSF 352
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 YDRLTLSAMNDGSFNPNVHIGYWDTPGSEATIEEAMDRLTDVFIERLNAYATSHVLDLGC 77
 STRANDEDNESS:
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                                   ENGTH:
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                   amino
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                                     282 amino acids
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                 acid
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relevant
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                                                                                                                                                                     30,617
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                                                                                                                                                     15280-216000
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                           Version #1.30
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TOPOLOGY:

US-09-036-987A-7

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US-09-041-718-3
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; ORIGINAL SOURCE:
; ORGANISM: Esc
US-08-457-245-9
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TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-041-718-3
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RESULT
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Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bard, Martin
TITLE OF INVENTION: DNA encoding sterol methyltransferase
FILE REFERENCE: 740.003US1
CURRENT APPLICATION NUMBER: US/09/041,718A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local :
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                                                                                            404 IRQRG---YDLHDVKAYGKMLKDAGFVEVIAENRTD 436
                                                                                                                                                                       348 PENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKS----AGTPSAEFAAY 403
                                                                                                                                                                                                                                                                                                                                                                                                             190 KECHMQDDSGNSYELSLIGCKCIGAYVKSKKNQNQ---ISWLWQKVDSEDDKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 SIGLKCAVEFEVADCTKKDYPE--NSFDVIYSRDTILHIQDK--PALFRSFHKWLKPGGK 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 VKSKKNONQISWLWQKVDSEDDKG---FQRFLDSSQYKFNSILRYERVFGPGYVSTGGLE 272
                                                       244 EIELGDGIPKMFHVDVARKALKNCGFEVLVSEDLAD
                                                                                                                                                                                                              124 LDVGCGVGGPAREIARFTGCNVIGLNNNDYQIAKAKYYAKKYNLSDQMDFVKGDFMKMDF 183
                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                          15 RELH-GDDIGKKTGLSAL------MSKNNSAQKEAVQKYLRNWDGRTDKDAEERRLE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 SAQQAKLKMICEKLQLKPGMRVLDIGCGWGGLAHYMASNYDVSVVGVTISAEQQKMAQER
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les 59; Conservative
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                                                                                                                                                                                                                                                     LDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEFEVADCTKKDY 347
                                                                                                                                                                                                                                                                                          DYNEATHSYYNVVTDFYEYGWGSSFHFSR-FYKGESFAASIARHEHYLAYKAGIQRGDLV 123
                                                                                                                                   EENTFDKVYAIEATCHAPKLEGVYSEIYKVLKPGGTFAVYEWVMTDKYDENNPEHRKIAY
                                                                                                                                                                                                                                                                                                                                 -----FQRFLDSSQYKFNSILRYERVFGPGYVSTGGLETTKEFVS-KLDLKPGQKV 289
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23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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Pred. No. 1.8e-08;
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0; Mismatches 69;
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RESULT 7
US-09-041-718-4
; Sequence 4, Application US/09041718A
; Patent No. 6225075
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (317)337~484
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0:
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Waldron, Clive TITLE OF INVENTION: Biosynthet TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS: LENGTH: 275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                        262 GP-----GYVSTGGLETTKEFVSKLD------LKPGQKVLDVGCGIGGGDFYMAENYD 308
                                                                                                                                                                 427 VEVI----AENRTDQFIQVLQKELDALEQEKDDFIDDFSEEDYNDIVDGWKA 474
                                                                                                                                                                                                                                                                                                                  309 VEVVGIDLSINMISFALE--RSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQD 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       29 GPCAIHHGYWENDGRASWQQAADRLTDLVAERTVLDGGVRLLDVGCGTGQPALRVARDNA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 28, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                              -EILDWEDVSSRTRYFMPQFAEELAAHQHGIAD----
                                                                                                                                                                                                                                          KPALFRSFHKWLKPGGKVLISDYCKSAGTPSAEFAAYIRQRGYDLHDVKAYGKMLKDAGF 426
                                                                                                                                                                                                      PDRAIREILRVLKPGGILGVTEVVKREAGGGMPVSGDRWPTGLRICLAEQLLESLRAAGF
                                                                                                                                                                                                                                                                               IQITGITVSQVQVAIAADCARERGLSHRVDFSCVDAMSLPYPDNAFDAAWAMQSLLEMSE 148
                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
57; Conserv
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Turner, Jan R.
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Crawford, Kathryn P.
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Pred. No. 1.7e-08;
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GENERAL INFORMATION:

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APPLICANT: Bard, Martin
TITLE OF INVENTION: DNA encoding sterol methyltransferase
FILE REFERENCE: 740.003US1
CURRENT APPLICATION NUMBER: US/09/041,718A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 9
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 361
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-041-718-4
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: Sequence 2, Application US/09041718A

: Patent No. 6225075
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 376 .
TYPE: PRT
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APPLICANT: Bard, Martin
TITLE OF INVENTION: DNA encoding sterol methyltransferase
FILE REFERENCE: 740.003US1
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Best Local 9
                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 NEYQVNRARLHNKKAGLDALCEVVCGNFLQMPFDDNSFDGAYSIEATCHAPKLEEVYAEI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GAYVKSKKNONQISWLW------OKVDSEDDKGFQRFLDSSQYKFNSILRYERV 260
                                                                                                                                                           53
                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                               KEFVS-KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERS----- 328
                                                                                                                                                                                              WOKVDSEDDKGFORFLDSSQ------YKFNSILRYERVFGPGYVSTGGLETT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKWLKPGGKVLISDYCKSAGTPSAEFAA----YIR-----QRGYDLHDVKAY----GKMLK 422
  KYHLDHKLSYVKGDFMQMDFEPESFDAVYAIEATVHAPVLEGVYSEIYKVLKPGG-----
                                   -IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLIS 387
                                                                            EHFLAHKMNLNENMKVLDVGCGVGGPGREITRFTDCEIVG----LNNNDYQIERANHYAK 166
                                                                                                                                                         WDGGISKDDEE-KRLNDYSQLTHHYYNLVTDFYEYGWGSSFHFSRYY-KGEAFRQATARH 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGPGYVSTGGLETTK----EFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDL 316
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24.0%;
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                                                                                                                                                                                                                                                          Score 148.5; DB 4; Pred. No. 2.3e-06;
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Pred. No. 1.6e-07
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RESULT 10
US-08-457-245-8
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APPLICANT: KIMURA, HİTOSHİ
APPLICANT: KIMURA, HİTOSHİ
APPLICANT: KIMURA, TATSUYA
APPLICANT: NAGAHASHİ, YOSHİE
TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: BİOTİN GENES: US/08/935,263A
CURRENT APPLICATION NUMBER: US/08/935,263A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: EP 96115540.5
EARLIER FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 23
SOFTWARR: Patentin Ver: 2.1
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US-08-935-263-16
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                                                                                                              GENERAL INFORMATION:
APPLICANT: BARRY III, Clifton E.
APPLICANT: YUAN, Ying
                                    TITLE OF INVENTION: (TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 276
ADDRESSEE: Townsend
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 EREVFKKYWIEHSVDLTVEAMMLDSQASDLDKVERPEVLSMLPPYEGK---SVLELGAGI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DKQLLSKRFSEH-----AKTYDAYA-NVQKNMAKQLVDLLPQKNSKQRINILEIGCGT 54
                                                                                                                                                                                                                                                                                                                                                                         IKTFQELHM-----SYE---
                                                                                                                                                                                                                                                                                                                                                                                                                TKIFKECHMQDDSGNSYELSLIGCKCIGAYVKSKKNQNQISWLWQKVDSEDDKGFQRFLD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFSNWLLMYLSDEEVERLVERMLKWLKPGGYIFFRESCFHQSGDHKRKSNPTHYREPRFY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYLTRLLVNTFPNASITAVDLAPGMVEVAKGITME-DRVTFLCADIEEMTLN---ENYDL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                     CLONING AND EXPRESSION OF DNA INVOLVED IN THE BIOSYNTHESIS OF CYCLOPROPANATED MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%; Score 128.5; DB 3; 22.9%; Pred. No. 0.00013; tive 45; Mismatches 97;
                                      21
and
Townsend Khourie
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US-08-457-245-8
5386025-8
                           ; SEQ
                                                                                                                                              ;Patent No. 5386025;
APPLICANT: JAY,
                                                                                                      M.; CAMPBELL, KEVIN P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
                             FILING DATE: ID NO:8:
                                                            NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                               460 FSEEDYNDI 468
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               LENGTH: 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSKLGLEPGMTLLDIGCGWGSTMLHAIEKYDVNVIGLTLSANQLAHN------KLKF 118
                                                                                                                                                                                                                                                                                                                                                                                                                  LKPGGKVLI-----SDYCKSAG--TPSA--EFAAYIRQRGYDLHDVKAYGKMLK----
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                                                                                                                                              SCOTT D.; ELLIS,
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                                                                                                                                              STEVEN B.; HARPOLD,
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                                                                                            APPLICATION NUMBER: US/08 FILING DATE: May 31, 1995 PRIOR APPLICATION DATA:
                                              FILING DATE: April 4, 1994 PRIOR APPLICATION DATA:
                                                                                                                                            SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brenner, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
FILING DATE: April 1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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               APPLICATION NUMBER: 07/868, FILING DATE: April 10, 1992
                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                         CITY:
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                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                            ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARFYVTDGGITRYYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTA--PYFNKSGPGAY 775
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Feldman, Daniel
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                                                                                                                                                                                         IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                       HUMAN CALCIUM CHANNEL COMPOSITIONS METHODS 57
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                                                                                                                                                                                                                                                                                                                         Martin,
                                                                                                                                                                                                                                                                                                                                                                                                      Robert
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

DATE:

15-AUG-1991

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LENGTH: 1084 amino aci
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FRAGMENT TYPE:
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                                     424 ----AGFVEVIAE------NRTDQFIQVL--QKELDALEQEKDDFIDDFSEE 463
                                                                                                                                                                                                     319 N-MISFALERSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKW 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 LNISPNSVDIIFSNWLLLMYLSDEEVERLVE-RMLKWLKP-----GGYIFF--RESC---- 163
894 GAGHRSAYVPSVADILQIGWWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 953
                                                                                                                                                                                                                                                                                     261 FGPGYVSTGGL--ETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSI 318
                                                                                                                                                                                                                                                                                                                             711 KARFVVTDGGITRVYPKEAGEN-----WQENPETYEDSFYKRSLDNDNYVFTA--PYFNK 763
                                                                                                                                                                                                                                                                                                                                                                  210 KC------IGAYVKSKKNQNQISWLWQK-VDSEDDKGFQRFLDSSQYKFNSILRYERV 260
                                                                                                                                                                                                                                                                                                                                                                                                            653 ISDNNTEFLLNFNEFIDRKTPNNPSCNAD--LINRVLLDAGFTNELVQNYWSKQKNIKGV 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 VNGTDYSLALVLPTYSFYYIKAKLEETITQARYSETLKPDNFEESGYTFIAPRDYCNDLK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 KSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTP 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 KASQVIALDFIESVIK-----KNESINGHYKNVKFMC-----ADVTSPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/US89/01408 FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 04-API
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELEPHONE:
                                                                                                                       LKPGGKVLIS---DYCKSAG-----TPS----AEFAAYIRQRGYDLHDVKAYGKMLKD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------FHQSGDHKRKSNPTHYREPRFYTKIFKECHMQDDSGNSY---ELSLIGC 209
                                                                               LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSVCEPGAAPKQ
                                                                                                                                                                 NSWIENFTKTSIRDPCA--GPVCDCKR----NS-DVM---DCVI----
                                                                                                                                                                                                                                             SGPGAYESGIMVSKAVEIYIQGKLLKPA-----
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amino acid
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internal
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04-APR-1989
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19.6%; Pred. No. 0.0075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/482,384
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                                                                                                                                                                                                                                         Indels
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Best Local Simi
Matches 94;
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                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 07/745,206
                                                                                                                                                   MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (619)238-0999
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100.
CITY: San Diego
CITY: San Diego
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SOFTWARE: FastSE
77 KASQVIALDFIESVIK-----KNESINGHYKNVKFMC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/868, FILING DATE: April 10, 1992
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                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/223,305C FILING DATE: April 4, 1994
                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 52516 (P519739)
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                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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Feldman, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US 07/620,250
30-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-1988
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19.6%;
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                                                                 Score 120;
Pred. No. (
                                                   Mismatches
                                                 0; DB 2; I
. 0.0075;
tches 158;
                                                                                Length 1084;
                    -----ADVTSPS 115
                                                 Indels 152;
                                                   Gaps
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US 07/482,384

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US-08-455-543A-53

; Sequence 53, Application US/08455543A

; Patent No. 5792846
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                                                APPLICATION NUMBER: 07/868,354
FILING DATE: APRII 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
                                                                                                                                     APPLICATION NUMBER: US/08/455,1
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: APril 4, 1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brenner,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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CTTY: San Diego
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                                                                                                                                                                                                                                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSVCEPGAAPKQ 893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNISPNSVDIIFSNWLLMYLSDEEVERLVE-RMLKWLKP----GGYIFF--RESC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSWIENFTKTSIRDPCA--GPVCDCKR----NS-DVM---DCVI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KARFVVTDGGITRVYPKEAGEN-----WQENPETYEDSFYKRSLDNDNYVFTA--PYFNK 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FHQSGDHKRKSNPTHYREPRFYTKIFKECHMQDDSGNSY---ELSLIGC 209
                                                                                                                                                                                                                                                                                                                                                            92101-2926'
                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                              1660 Union
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Ellis, S
                                                                                                                                                                                                                                                                   FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCue, Ann
                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown, Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -IGAYVKSKKNONOISWLWOK-VDSEDDKGFORFLDSSQYKFNSILRYERV 260
30-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROBERT
HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael
                                                                                                                                                                                                                                                                                       Sod
                  us 07/620,250
                                                                                                                                                                                                                                                                                                                                                                                                                              Street
                                                                                                                                                                                                                                 US/08/455,543A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Haller & McClain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVGIKIDV
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Best Local Similarity 19.0
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619)238-0062 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 20-FEB-PRIOR APPLICATION DATA:
913
                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 04-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
GAGHRSAYVPSVADILQIGWWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ
                                                                    LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSVCEPGAAPKQ
                                                                                                                                                                          N-MISFALERSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIODKPALFRSFHKW 377
                                                                                                                                                                                                             SGPGAYESGIMVSKAVEIYIQGKLLKPA--
                                                                                                                                                                                                                                                FGPGYVSTGGL--ETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSI 318
                                                                                                                                                                                                                                                                                                                   KC-----IGAYVKSKKNQNQISWLWQK-VDSEDDKGFQRFLDSSQYKFNSILRYERV 260
                                                                                                                                                                                                                                                                                                                                                        ISDNNTEFLLNFNEFIDRKTPNNPSCNAD--LINRVLLDAGFTNELVQNYWSKQKNIKGV 729
                                                                                                                                                                                                                                                                                                                                                                                         ------FHQSGDHKRKSNPTHYREPRFYTKIFKECHMQDDSGNSY---ELSLIGC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNISPNSVDIIFSNWLLMYLSDEEVERLVE-RMLKWLKP-----GGYIFF--RESC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTP 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KASQVIALDFIESVIK-----KNESINGHYKNVKFMC----
                               ----AGFVEVIAE-----
                                                                                                     LKPGGKVLIS---DYCKSAG-----TPS----AEFAAYIRQRGYDLHDVKAYGKMLKD
                                                                                                                                         NSWIENFTKTSIRDPCA--GPVCDCKR----NS-DVM---DCVI------
                                                                                                                                                                                                                                                                                  KARFVVTDGGITRVYPKEAGEN-----WQENPETYEDSFYKRSLDNDNYVFTA--PYFNK 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 120; DB 1;
19.6%; Pred. No. 0.0077;
tive 76; Mismatches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,779
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                         ---NRTDQFIQVL--QKELDALEQEKDDFIDDFSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                               -VVGIKIDV
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 972
                                   463
                                                                      912
                                                                                                         423
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                                                                                                                                          852
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26;

RESULT 15
US-08-223-305C-53
; Sequence 53, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:

APPLICANT:

Harpold, Michael Ellis, Steven

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                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-08-223-305C-53
                                                                                                                                                                 Query Match
Best Local Similarity 19.6
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: Liskette

COMPUTER: Liskette

COMPUTER: Liskette

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 14, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

APILICATION NUMBER: US 07/745,206

FILING DATE: 30-NOV-1990

PRIOR APPLICATION NUMBER: US 07/620,250

FILING DATE: 20-FEB-1990

PRIOR APPLICATION NUMBER: US 07/482,384

FILING DATE: 04-APR-1989

PRIOR APPLICATION NUMBER: US 07/603,751

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION NUMBER: WO 07/603,751

APPLICATION NUMBER: WO 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION NUMBER: WO 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION NUMBER: WO 07/603,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/ACENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCue, Ani
APPLICANT: Brenner, I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
612 VNGTDYSLALVLPTYSFYYIKAKLEETITQARYSETLKPDNFEESGYTFIAPRDYCNDLK 671
                           116 LNISPNSVDIIFSNWLLMYLSDEEVERLVE-RMLKWLKP-----GGYIFF--RESC---- 163
                                                                                         552 KSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTP 611
                                                                                                                                   77 KASQVIALDFIESVIK-----KNESINGHYKNVKFMC------ADVTSPS 115
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
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CITY: San Diego
STATE: Californ:
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1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1103 amino acids
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Feldman, Daniel
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57
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                                                                                                                                                                                       76;
                                                                                                                                                                                     Score 120; DB 2; Length 1103;
Pred. No. 0.0077;
76; Mismatches 158; Indels 15
                                                                                                                                                                                  Indels 152; Gaps
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26;

972	913 GAGHRSAYVPSVADILQIGWWATAAAWSILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 972	913	В
463	NRT	424	Qy
912	853 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNISVYAFNKSYDYQSVCEPGAAPKQ 912	853	Db
423	378 LKPGGKVLISDYCKSAGTPSAEFAAYIRQRGYDLHDVKAYGKMLKD 423	378	Qy
852	819 NSWIENETKTSIRDPCAGPVCDCKRNS-DVMDCVI 852	819	DЬ
377	319 N-MISFALERSIGLKCAVEFEVADCTKKDYPENSEDVIYSRDTILHIQDKPALFRSFHKW 377	319	Qy
818	783 SGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDV 818	783	Ъ
318	Æ	261	Qy
782	730 KARFVVTDGGTTRVYPKEAGENWGENPETYEDSFYKRSLDNDNYVFTAPYFNK 782	730	В
260	210 KCIGAYVKSKKNQNQISWLWQK-VDSEDDKGFQRFLDSSQYKFNSILRYERV 260	210	Qy ·
729	672 ISDNNTEFLLNENEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGV 729	672	В
209	164FHQSGDHKRKSNPTHYREPRFYTKIFKECHMQDDSGNSYELSLIGC 209	164	Qy

Search completed: September 20, 2001, 16:19:43 Job time: 181 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2001, 16:17:22; Search time 17:12 Seconds (without alignments)
2198.027 Million cell updates/sec

Title: US-09-525-885-2
Perfect score: 2598
Sequence: 1 MAASAMGVLQEREVFKKYWI.......KLVRTTEGEQOWGLFIAKKM 494,

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	0,		4	ω	2	ᆫ	No.	Result
160	161.5	162.5	163.5	165.5	166	170	170.5	171	173	174.5	175.5	176	176	176.5	177	182	182	183.5	185	187.5	189.5	191	204.5	207	449.5	498.5	1287.5	2086	Score	
			6.3			÷		6.6		6.7						7.0	7.0	7.1	7.1	7.2	7.3	7.4	7.9	8.0	17.3	19.2	49.6	80.3	Match L	% Query
361	378	581	254	366	389	383	283	389	346	227	283	382	382	306	348	344	344	462	318	227	387	367	317	363	495	437	374	555	Length	
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S63686	T39579	F84657	в72316	T33885	B71865	\$42003	JC6531	H64571	T10173	C75210	T44579	F85773	A44292	S18533	C96673	T04138	T01572	B75306	S76226	C71246	A81324	T06780	S76618	T06795	T27936	T29330	F96525	н96762	ID	
24-sterol C-methyl	sterol methyltrans	hypothetical prote	conserved hypothet	hypothetical prote	cyclopropane-fatty	24-sterol C-methyl	avermectin B 5-0-m	cyclopropane-fatty	24-sterol C-methyl	sterol biosynthesi	C5-O-methyltransfe	cyclopropane fatty	propane-fa	eryG protein - Sac	gamma-tocopherol m	24-sterol C-methyl	24-sterol C-methyl	\mathbf{L}		hypothetical prote	cyclopropane-fatty	ໝ	hypothetical prote	ເລ		hypothetical prote		hypothetical prote	Description	

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30
149	149	149.5	150	150.5	150.5	151	151	154.5	156	156.5	156.5	156.5	157.5	159.5	159.5
5.7	5.7	5.8	5.8	5.8	5.8	5.8	5.8	5.9	6.0	6.0	6.0	6.0	6.1	6.1	6.1
251	245	256	776	262	218	352	273	278	379	394	324	253	269	391	286
Ν	N	N	Ŋ	Ŋ	Ŋ	Ŋ	N	N	N	2	N	N	N	N	Ŋ
A86071	в86738	F85505	B70797	S62195	H84364	T03845	T34740	T38024	T50969	C82951	T42375	F83511	C75569	T08338	B70614
hypothetical prote	hypothetical prote	unknown [imported]	probable transfera	hypothetical prote	membrane protein [probable 24-sterol	hypothetical prote	hypothetical prote	probable DELTA(24)	conserved hypothet	probable 24-sterol	hypothetical prote	probable methyltra	conserved hypothet	probable mmaAl pro

ALIGNMENTS

RESULT 1 H96762 hypothetical protein F6D5.1 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: H96762 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marzia A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719 A; Accession: H96762 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-555 <sto> A; Creose-references: GB:AE005173; NID:g10092368; PIDN:AAG12776.1; GSPDB:GN00141 A; Map position: 1 A; Map position: 1</sto>

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C;Dates 02: Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Dates 02: Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F95525
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta.; Ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Rocession: F95525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 < STD.
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Best Local Similarity
Matches 243; Conserv
                     488
                                                             308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIFKECHMQDDSGNSYELSLIGCKCIGAYVKSKKNQNQISWLWQKVDSEDDKGFQRFLDS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEVIAENRTDQFIQVLQKELDALEQEKDDF 456
                                                                                                                                                                                                                                            FEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKSAGTP 396
                                                                                                                                                                                                                                                                                                                            FVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERSIGLKCAVE 336
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                                                             ISDFSEVKTFLTTNSFEQNTCLLCSHIDHKILLLQEDYNDIVGGWSAKLERTASGEQKWG
                                                                                                     IDDFSE----
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                                                                                                                                                                                                                         FEVADCTTKTYPDNSFDVIYSRDTILHIQDKPALFRTFFKWLKPGGKVLITDYCRSAETP
                                                                                                                                                                                                                                                                                                         FVAKMDLKPGQKVLDVGCGIGGGDFYMAENFDVHVVGIDLSVNMISFALERAIGLKCSVE
                                                                                                                                                                                                                                                                                                                                                                                       VQYKSSGILRYERVFGEGYVSTGGFGNSILTLLSSYGHTYLYCLSVIFMFLFSLTETTKE 127
                                                                                                                                                                                                                                                                                                                                                                                                                           SQYKFNSILRYERVFGPGYVSTGGL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVFQECQTRDASGNSFELSMVGCKCIGAYVKNKKNQNQICWIWQKVSVENDKDFQRFLDN 67
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                                                                                                 -----EDYNDIVDGWKAKLVRTTEGEQQWG
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                                                                                                                    hypothetical protein ZK622.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: C-Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T27936 R;Leimbach, D. Submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid ZK62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, July 1996
submitted to the sequence of C. elegans cos
A; Molecule type: DNA
A; Residues: 1-495 <L
A; Cross-references:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                      A;Accession: T27936
A;Status: preliminary; translated
                                                                                                 A; Description: The sequence A; Reference number: Z20443
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A;Map position: 5
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A; Residues: 1-437 < PAU>
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les 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKDYPENSEDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKSAGTPSAEFAAY 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKKVFAPTTDATITERDFLDKTQYTNTGIDAYEWMFGVNFISPGGYDENLKIIKRFGDFK 223
                                                                                                                                                                                                                                                                                                                                               ERDSLISGWIDKLGYIEKDNHNWNFFLAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRQRGYDLHDVKAYGKMLKDAGFVEVIAENRTDQFIQVLQKELDALEQEKDDFIDDFSEE 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QKV---DSEDDKGFQRFLDSSQYKFNSILRYERVFGPGYVSTGGLETTKEFVSKL-DLK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADVLIFNNALSQIITNADL-----LTDFLKNATNATAIGGTVIIRED-LKDCSDKRQV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36/2;
                   1-495 <LEI>
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                                                                                                                                                                                                      #sequence_revision 15-Oct-1999 #text_change
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e: strain Bristol N2; clone F54D11
  EMBL: U39998;
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  PIDN: AAA81102.1;
                                                             from GB/EMBL/DDBJ
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Pred. No. 1.7e-27;
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    CESP: 2K622
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C;Genetics:
A;Gene: MT1
A;Gene: MT1
C;Superfamily: 24-sterol C-methyltransferase; bioC homology
C;Keywords: methyltransferase; S-adenosylmethionine
F;120-224/Domain: bioC homology <BIOC>
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A;Gene: CESP:ZK622.3
A;Introns: 34/2; 97/2; 222/3; 310/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK622.3
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                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-363 <SUB>
                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: 215820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable 24-sterol C-methyltransferase (EC 2.1.1.41) - N; Alternate names: delta-24-sterol methyltransferase
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                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U60754; NID:g1706964; PIDN:AAB37769.1;
                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Subramaniam,
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Date: 23-Apr-1999
;Accession: T06795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Triticum aestivum (common wheat);Date: 23-Apr-1999 #sequence_revision 23-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 137;
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Best Local :
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                                    280 KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMIS--FALERSIGLKCAVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GELAEKASQVIALDFIESVIKKNESINGHYKNVKFMCADVTSPSLNISPNSVDIIFSNWL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVLAETARWVLSTDFIDSFIKKNQERNAHLGNINYQVGDAV--GLKMESNSVDLVFTNWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYINLLRAIRYRDVDNKLWRFNVQWSCSVPTYIKRSNNWRQVHWLAEKVPAEDGAKGTSF
QLELKPGMKVLDVGCGIGGPLREIARFSSTSVTGLNNNDYQITRGKALNRSVGLGATCDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEVIAENRTDQFIQVLQKELDALEQEKDD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPRTVSPYCHINA - - HTLAETFNANVWNTEIIPEYYRTSLTKSNNLKDQRVRFGWNQSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERSIGLK-CAVEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NELVELIKNTWQNEQEAWDAKLDDEK-----YV-----WTDKVFSSALTSLPSNSTFFLY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRFLD-----SSQYKFNSILRYERVFGPGYVSTGGLETTKEFVSKLDLKPGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYTKIFKECHMQDDSGNSYELSLIGCKCIGAYVKSKKNQNQISWLWQKVDSEDD-KG--F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMYLSDEETVEFIFNCMRWLRSHGIVHLRESCSEPSTGRSKAKSMHDTANANPTHYRFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMYLSDEEVERLVERMLKWLKPGGYIFFRESCFHQS-GDHKRKS-----NPTHYREPR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANFKSFWDKYSDKPDTNSMMLNHSAEELESSDRADILASLPLLHNKDVVDIGAGIGRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVTYWQQKD---ALFDVFVATEFLSTVDDE--TIRQLPNVMSDGAKFITLEPVDEVN--
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28.6%;
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28.6%;
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                                                                                                Score 207; DB 2;
Pred. No. 4.1e-07;
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                                                                               Mismatches
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                                                                                                                   Length 363
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hypothetical protein - C; Species: Synechocyst A; Variety: PCC 6803 C; Date: 25-Apr-1997 #s C; Accession: S76618 R; Kaneko, T.; Sato, S.
                         A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-367 <SHI>
                                                                                                                   R;Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K. J. Biol. Chem. 271, 9384-9389, 1996
A;Title: Identification and characterization o A;Reference number: Z15807; MUID:96199190
                                                                                                                                                                                                                                                              probable 24-sterol C-methyltransferase (EC 2.1.1.41) - soybean
N;Alternate names: S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase
C;Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D64004; GB:AB001339; A;Note: the nucleotide sequence was submitted C;Superfamily: bloc homology CBIOC> F;95-199/Domain: bloc homology CBIOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Syr
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C;Accession: T06780
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A; Residues: 1-317 <KAN>
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Best Local S
Matches 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISD 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                         200 WCHRPIDPGNGPLTADERRHL-QAIYDVYCLPYVVSLPDYEAIARECGFGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 YC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 KELLAWAVPQNSAKP-RKILDLGCGIGGSSLYLAQQHQAEVMGASLSPVQVERAGERARA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 YEKIKNFYDDSSGLWEDVWGE------HMHHGYYGPHGTYRIDR------RQAQIDLI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSLSSFRLTTVGRIITRNMVKVL--EYVGLAPEGSQRVSSFLEKAAEGLVEGGKKEI 348 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEF----VSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALE--RS 328
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EMBL: U43683; NID: g1399379; PIDN: AAB04057.1;
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26.38;
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                                                                                                                      characterization of MUID:96199190
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Pred. No. 5.1e-07;
48; Mismatches 90;
                                                                         from GB/EMBL/DDBJ
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                                                                                                                                               S-adenosyl-L-methionine:
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A; Cross-references:

PID:g1399380

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A81324
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-387 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The genome sequence of the food-borne pathogen Campylobacter A;Reference number: A81250; MUID:20150912 A;Accession: A81324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, Andrew 403, 665-668, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                        ;Gene: cfa; Cj1183c
;Superfamily: cyclopropane-fatty-acyl-phospholipid synthase; MCM homology
;Reywords: methyltransferase; phospholipid metabolism; S-adenosylmethionine
                                                                                                                                                                                                                                    Matches
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Best Local
  197
                                                                                                                                                                                          215 YVKSKKNONQISWLWQKVDSEDDKG-----FQRFLDSSQ-----YKFNSILRYERV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 YVSTGGLETTK----EFVSK-----
                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 7.4%;
Local Similarity 22.5%;
tes 81; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KKKKNRNEV----VLCSAEGTGGCSRLAAMDLASNLGGKIDKAEV-LSAVQKYEKY----
CKKAKERVKELGLEDKIEIRLQNYQDLEF
                                      ISFALER--SIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHI--QDKPALFRSFHK 376
                                                                                                                FGPGYVSTGGLETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINM
                                                                                                                                                      FFKTKK--DVLSKITQKQESKNIKSHYDIGNDFYKLWLDDTMSYSCAYFKEPNNTLYE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSHFSLSSFRLTAVGRLFTKNMVKVL--EYVGLAPKGSLRVQDFLEKAAEGLVEGGKREI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQNPEHQKIKAEIEIGDGLPDIRLTAKCLEALKQAGF-EVIWEKDLAVDSPLPWYLPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TPSAEFAAYIRQRGYDLHDVKAYGK---MLKDAGFVEVIAENR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLQLGLKPGQKVLDVGCGIGGPLREISRFSSTSITGLNNNEYQITRGKELNRIAGVDKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVCYGGQEEERKANYTDMVNKYYDLVTSFYEFGWGESFHFAPRWKGESLRESIKRHEHFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFVKADFMKMPFPDNSFDAVYAIEATCHAPDAYGCYKEIFRVLKPGQYFAAYEWCMTDSF
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                                                                                                                                                                                                                                    73;
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                    Conservative
                                                                          -AQINKIEHTLKKLDLKEGEKLLDIGCGWGWLSIMAAQKYGVKVVGITISEEQ 196
                                                                                                                                                                                                                                                    7.3%;
24.7%;
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                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                                                       ; GB:AL111168; NID:g6968444; PIDN:CAB73437.1; O2, strain NCTC 11168
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                                                                                                                                                                                                                                                  Score 189.5;
Pred. No. 7.5
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Pred. No. 5.5e-06;
8; Mismatches 119
                                                                                                                                                                                                                                  Mismatches
-ENYFDKVVSVGMFEHVGKENLGLYFMKVKQ
                                                                                                                                                                                                                                                    5; DB 2;
7.5e-06;
                                                                                                                                                                                                                                  115;
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                                                                                                                                                                                                                                                                        387;
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                                                                                                                                                                                                                                  51;
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Whitehead, S
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S.; Barre
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123

QVFKEVRRVLKPSGKFIM

369 ALFRSFHKWLKPGGKVLI 386

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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: C71246
                                                                                                                                                                                                                                                                                 C;Superfamily: conserved hypothetical protein F;39-144/Domain: bioC homology <BIOC>
                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain OT3 A; Note: this accession replaces an
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-227 <K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.; Ohfuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and
                                                                                                                                                                                                                                                                                                                                 A; Gene: PH0226
                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29298.1; PID:g3256615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A71000; A; Accession: C71246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haika
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein PH0226 - Pyrococcus horikoshii
                                                                                                                                                                                               Query Match
Best Local
                           311 VYGIDLSINMISFALERSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQ--DKP 368
                                                                                                                               257 YERVFGPGYVSTGG-----LETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVE 310
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  63
                                                                                      6 YYRVF-PTYTDINSQEYRSRIETLEPLLMKYMKKRG-KVLDLACGVGGFSF-LLEDYGFE 62
VVGVDISEDMIRKAREYAKSRESNVEFIVGDARKLSFEDKTFDYVIFIDSIVHFEPLELN 122
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                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1-227 <KAW>
                                                                                                                                                                                               Similarity
                                                                                                                                                                          Conservative
                                                                                                                                                                                          7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and gene organization of the MUID:98344137
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                                                                                                                                                                                               Score 187.5; DB 2
Pred. No. 5.1e-06;
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A; Note: the nucleotide sequence C; Superfamily: bioC homology F; 94-195/Domain: bioC homology <
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C;Accession: S76226
R;Kaneko, T.; Sato,
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein - Synechocystis sp. C;Species: Synechocystis sp. A;Variety: PCC 6803
                                            A; Cross-references: EMBL:D90914; GB:AB001339; A; Note: the nucleotide sequence was submitted
                                                                                    A; Molecule type: DNA
A; Residues: 1-318 <KAN>
                                                                                                                                A; Status: preliminary
                                                                                                                                                          A; Accession: S76226
                                                                                                                                                                               A; Reference number:
                                                                                                                                                                                                                            A; Title: Sequence analysis of the genome of
                                                                                                                                                                                                                                                   DNA Res. 3,
                                                                                                                                                                                                                                                 Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wa
A Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                        #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                  S74322;
                                                                                                                                                                                  MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                            (strain PCC
                                                                                                                                                                                                                            the unicellular cyanobacterium
                                            NID:g1653477; PIDN:BAA18485.1; PID:d101 to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                           Wada,
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/ada, T.; W
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<BIOC>

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RESULT
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 24-sterol C-methyltransferase (BC 2.1.1.41) - maize
N;Alternate names: (S)-adenosyl-methionine:delta
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 *sequence_revision 19-Feb-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cyclopropane-fatty-acyl-phospholipid synthase - Deinococcus radiodurans
C;Speciles: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75306
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Best Local
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                                                                                                                                                                                                                                 342
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                                                                                                                                                                                         451 QEKDDFIDDFSEEDYNDIVDGWKAKL-----VRTTEGEQQ---WGLFI 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 -PPDVTAKFAVDDAMALSFPDGSFDVVWSVEAGPHMPDKAVFAKELLRVVKPGGILVVAD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 GGLETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 34.7 nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR2187
                                                                                                                                                                                                                               VPMWLQSGNFA----RKYVFPD----GELLP----VWETLKYASEQLFEV--RDVENL-
                                                                                                                                                                                                                                                           TP----SAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEVIAENRTDQFIQVLQKELDALE
                                                                                                                                                                                                                                                                                                                                                                                  RLLDIGCGWGGLSLYAAQHYGVQVLGVTLSQAQLQEGQARVRVAGLEGQVQLEL-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQQAIQYHYDVSNDFYKLWLDERMVYSCAYF-PGGQETLDEAQTAKLDYICRKLQLRPGE
                                                                                                                                                                                                                                                                                                        DYRDVLSRGPAQFDKIASVGMAEHVGRRNMPEYFRSAYAALKPGGLMLNHAIGDGIGQAR
                                                                                                                                                                                                                                                                                                                                            DYPE-----NSFDVIYSRDTILHI--QDKPALFRSFHKWLKPGGKVL---ISDYCKSAG
                                                                                                                                                                                                                                                                                                                                                                                                                      KVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMI--SFALERSIGLKCAVEFEVADCTKK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
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                                                                                                                                                     REHYALTIGHWAARLEAHRPEALALLGEERLRLWRLYL 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.18;
27.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 185; DB 2; I
Pred. No. 1.2e-05;
2; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 183.5; DB 2
Pred. No. 2.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: g6459976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
#text_change
                                   24-sterol methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 318;
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   05-May-2000
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T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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EVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYC-KSAGTP QLGLKPGMKVLDVGCGIGGPLREIARFSSTSVTGLNNNEYQITRGKELNRLAGISGTCDF 154

95

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submitted to the EMBL Data Library
A; Reference number: Z14350
A; Accession: T01572
A; Status: preliminary; translated
                                                                                                                                                                   C;Function:
A;Description: methyltransferase
A;Description: methyltransferase; bioC l
C;Superfamily: 24-sterol C-methyltransferase; bioC l
C;Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. 34, 891-895, 1797, A;Title: Characterization of zea-mays endosperm C-24 A:Reference number: Z09668; MUID:97435974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: 24-sterol C-methyltransferase; bioC homology C;Keywords: methyltransferase; S-adenosylmethionine F;101-205/Domain: bioC homology <BIOC>
                                                                                                                                                  C; Keywords: methyltran: F; 101-205/Domain: bioC
                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T04138
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Grebenok, R.J.; Galbraith, Plant Mol. Biol. 34, 891-896,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-sterol C-methyltransferase (EC 2.1.1.41) ESMT1, N;Alternate names: C-24 sterol methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF045570;
A;Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Tong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                     A; Gene: ESMT1
                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                        A; Experimental source: endosperm
                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-344 <GR
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-344 <TON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species:
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Best Local
                                                     Matches
280 KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 VKADFMKMPFDDNTFDAVYAIEATCHAPDPVGCYKEIYRVLKPGQCFAVYEWCVTDHYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSLSSFRLTSVGRMITRTMVKAL--EYVGLAPQGSERVSSFLEKAAEGLVEGGKKEI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNATHKRIKDEIELGNGLPDIRSTRQCLRAVKDAGFEVVWDKDLAEDSPLPWYLPLDPSR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAEFAAYIR---QRGYDLHDVKAYGKML---KDAGFVEV----IAENR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKSAG-TP 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                               1-344 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galbraith, D.W.; Dellapenna,
                                                                                                                                                                                                                                                                                                         EMBL: U79669; NID: g1899059; PIDN: AAB70886.1; PID: g1899060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (maize)
                                                                                                                                                  homology <BIOC>
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                                                                    7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDQFIQVLQKELDALEQEKDDFIDDFSEEDYNDIVDGWKAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library,
                                                     41;
                                                   Score 182; DB 2; Pred. No. 2.2e-05; DB; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 182; DB 2; L
Pred. No. 2.2e-05;
Pred. No. 2.3e-05;
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                                                                                                                                                                                         bioC homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #text_change 11-May-2000
                                                                                    Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                            sterol methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
                                                   Indels
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                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476
                                                 Gaps
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                337
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gamma-tocopherol methyltransferase [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 **sequence_revision 02-Mar-2001 **text_change 31-Mar-2001 C;Accession: C96673 **R.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Consen, N.F.; Hughes, B.; Hulzar, L. A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Mooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference number: A86141; MUID:21016719 A;Accession: C96673
                                                                                                                  eryG protein - Saccharopolyspora erythraea
C;Species: Saccharopolyspora erythraea
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 22-Oct-1999
C;Accession: S1853; S16747
R;Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Lead
Mol. Gen. Genet. 230, 120-128, 1991
methyltransferases.
A; Reference number:
A; Accession: S18533
                                                         Mol. Gen. Genet. 230, 120-128, איז איז Genes involved in erythromycin biosynthesis A;Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis
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A; Residues: 1-348 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005173; NID:g8099780; PIDN:AAD38271.2; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 GKVLISDYCK---SAG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 ANDLAAAQSLAHKASFQVADALDQPFEDGKFDLVWSMESGEHMPDKAKFVKELVRVAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 A--LERSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 NETSGLWEEIWGDHMHHGFYDPDSSVQLSDSGHKEAQIRMIEES-----LRFAGV--- 118
                                                                                                                                                                                                                                                                                                                                                                                                                     GRIIIVTWCHRNLSAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYVSTGGLETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TDEEEEKKI-----KKVVDVGCGIGGSSRYLASKFGAECIGITLSPVQAKR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQISWLWQKV-----DSE---DDKGFQ----RFLDSSQYKFNSILRYERVFGP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAEFAAYIR --- QRGYDLHDVKAYGKML --- KDAGFVEV ---- IAENR ---- 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                 S18530; MUID:92079886
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27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                 J.; Leadlay,
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A;Gene: eryG
A;Start codon: GTG
C;Superfamily: bioC homology
F;82-187/Domain: bioC homology <BIOC>
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                                                                                                                                                                                                                                                                                        Q
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Matches
228
                                   418 GKMLKDAGEVEV-----IAENRTDQFIQVLQKE 445
                                                                                                                      374 FHKWLKPGGKVLISDYCK-----SAGTPSAEFAAYIRQRGYDLH------DVKAY 417
                                                                                                                                                               113 LTPSHVRIASERAERENVQDRLQFKEGSATDLPFGAETFDRVTSLESALHYEPRTDFFKG 172
                                                                                                                                                                                                         316 LSINMISFALERS--IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRS 373
                                                                                                                                                                                                                                                                         264 GYVSTG--GL-ETTKEFVSKL----DLKPGQKVLDVGCGIGGGDFYMAE-NYDVEVVGID 315
                                                                                                                                                                                                                                                   53 GYWKPGCAGLEEANQELANQLAEAAGISEGDEVLDVGFGLGAQDFFWLETRKPARIVGVD 112
AKQLREAGFVDVEVKSVRDNVMEPWLDYWLRKLQDE
                                                                            AFEVLKPGGVLAIGDIIPLDLREPGSDGPPK----LAPQRSGSLSGGIPVENWVPRETY
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Pred. No. 4.5e-05;
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Search completed: September 20, 2001, 16:20:09 Job time: 167 sec

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Maximum Match 100%
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ντην· ς-	THE REPLA	(1996).	he 28.0-	, Horiuchi T.;	J., Take	Nakade S., Nakamura	O K., Mi	Fujita I	PubMed=		8-1474(1997).					9	Richter G.		020-1102	y acid s	PubMed=	, SEQUI		ccerta;	A. La coli.	Y ACID	-ACYL-PI	25, Crea 25, Last		NDARD:			1294 · 1 700 1						
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C-METHIOTHER + DHO	TED FATT	GROUP FROM S-ADEN	on the	2014	Takeuchi Y., Wada C.	, Nashimoto H., Ni	., Mizobuchi K., Mori H.,	K., Inada T.,				richia coli K-	.D., Rode C.K., 1., Goeden M.A.,	C.A., Perna N.T		ייים מיייל מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מייים מיי	Werner T.,		:	f Escherichia coli:	. Jr.;	, AND CHARACTERIZATION		subdivision; Enteropacteriaceae;		HASE).) E (EC 2.	update)		381 AA	ALIGNMENTS	CITY	MVM	TJA	AST	LPJ	Id V	ERWHE	
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-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + PHOSPHOLIPID

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01-OCT-1994 (Rel. 31, Last sequence update)
01-CCT-1995 (Rel. 34, Last annotation update)
DELTA(24)-STEROL C-METHYLTRANSFERASE (EC 2.1.1.41).
ERG6 OR SED6 OR ISE1 OR LIE1 OR YML008C OR YM9571.10C.
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                                  SEQUENCE FROM N.A.

MEDLINE-94262330; PubMed-8203167;

Hardwick K.G., Pelham H.R.B.;

"SED6 is identical to ERG6; and en

required for ergosterol synthesis.

Yeast 10:265-269(1994).
                                                                                                                                                                                                               P25087;
01-MAY-1992
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                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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  SEQUENCE FROM N.A. MEDLINE-94312403;
                                                                                                                    NCBI_TaxID=4932;
                                                                                                                               sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of PDR4, a Saccharomyces cerevisiae gene that confers pleiotropic drug resistance in high-copy number: identity with YAP1, encoding a transcriptional activator."; Gene 101:149-152(1991).
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Gentles S., Bowman S., E
Submitted (JUN-1995) to
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-I CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 5-ALPHA-CHOLESTA-
-II REBN-3-BTRA-OL - S-ADENOSYL-L-HOMOCYSTEINE + 24-METHYLENE-
5-ALPHA-CHOLEST-8-EN-3-BETA-OL
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                        PENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKS----AGTPSAEFAAY
                                                                              LDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAVEFEVADCTKKDY
                                                   LDVGCGVGGPAREIARFTGCNVIGLNNNDYQIAKAKYYAKKYNLSDQMDFVKGDFMKMDF
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CONFLICT 55 63 NHENESEED -> SYPGDPLES (IN SEQUENCE 378 AA; 42867 MW; FA4D3D82A1CE03D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomycetales; Schizosaccharomyces.
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Pfam; PF01209; Ubie_methyltran; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98162722; PubMed=9501991; Yoshioka S., Kato K., Nakai K., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 55-378 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE DELTA(24)-STEROL SPBC16E9.05.
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                         376
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CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 5-8,24-DIEN-3-BETA-OL = S-ADENOSYL-L-HOMOCYSTEINE 5-ALPHA-CHOLEST-8-EN-3-BETA-OL.
                                                                                                                                                                                                                                                                  QSRKLQEYFEF-WDRNHENESEEDRARRIDGYKSVVNSYYDLATDLYEYGWSQSFHFSR-
                         KWLKPGGK - - - -
                                                                                                                                                                                                                  FGPGYVSTGGLETTKEFVS-KLDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSIN 319
                                                                    QISRCNNYAVKRNLDKKQV--FVKGDFMHMPFEDNTFDYVYAIEATVHAPSLEGVYGEIF
                                                                                                                    MIS----FALERSIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFH
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                                                                                                                                                                    FYKGEAFAQSIARHEHYLAYRMGIKPGSRVLDVGCGVGGPAREITEFTGCNLVGLNNNDY
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                      -VLISDYCKSAGTPSAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEV
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EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                   Score 161.5; DB
Pred. No. 0.0001
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NE + 24-METHYLENE-
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ero6 mutants.";
                                                                                                                                                                                                                                                                                                Sterol biosynthesis; Transferase; Methyltransferase. SEQUENCE 376 AA; 43085 MW; 369D094AFCDEDOAO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                 entities
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Eukaryota; Fungi; Ascomycota;
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15-JUL-1999
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                                                   DYCKSAGTPSAEFAAY -- IRQRGYD----LHDVKAYGKMLKDAGFVEVIAENRTDQFIQV
                                                                            KYHLDHKLSYVKGDFMQMDFEPESFDAVYAIEATVHAPVLEGVYSEIYKVLKPGG-----
                                                                                                                                                                                WDGGISKDDEE-KRLNDYSQLTHHYYNLVTDFYEYGWGSSFHFSRYY-KGEAFRQATARH 110
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                         ------IFGVYEWVMTDKYDETNEEHRKIAYGIEVGD-GIPKMYSRKVAEQALKN
                                                                                              -IGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLIS
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                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disruption,
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. C-METHYLTRANSFERASE (EC 2.
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24.0%;
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                                                                                                                                                                                                                                               Score 148.5; DB Pred. No. 0.0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.A.,
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                                                                                                                                                                                                                                   Mismatches
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(EC 2.1.1.41).
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susceptibility
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+ 5-ALPHA-CHOLESTA-
INE + 24-METHY
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270 VGFE---IEYQKD--LADVDDE

286

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RESULT 6
UBIE_ECOLI
ID UBIE_E
AC P27851
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Best Local :
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  UBIE_ECOLI
P27851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168 / BGSC1A1;
MEDLINE=96093926; pubMed=7584049;
Yoshida K.-I., Seki S., Fujimura M., Miwa
"Cloning and sequencing of a 36-kb region
genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO E.COLI YAFE.
-!- SIMILARITY: TO METHYLTRANSFERASES.
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                                                                                QNDQSTDHEIESVT---
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                                                                                                         KDDFIDDFSEEDYNDIVDGWKAKLVRTTEG
                                                                                                                                   EYFRFVREAFEESYSFEDIHQF----VQDAGIPNYSLETFHFLPEDFIESLDELEDAPLWE
                                                                                                                                                              EFAAYIR--
                                                                                                                                                                                                                 PENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLISDYCKSAGT----
                                                                                                                                                                                                                                            IDMGTGPGYLSIQLAKRTNAHVHAVDINPAMHEIAQEEAKKSGVSSLISFDLEDVHHLSY
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                                                                                                                                                                                                                                                                                               ITAEECRTYKEFVDLYQSYLYPLLGARLSRMYSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01209; Ubie_methyltran;
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000339;
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L 28.2
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               STANDARD;
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39, Last annotation update)
KDA PROTEIN IN ALDX-ASNH INTERGENIC REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                    28222 MW;
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Pred. No. 0.
               PRT;
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the Bacillus
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283 LKPGQKVLDVGCGIGG--GDFYMAENYDVEVVGIDLSINMISFALE--RSIGLKCAVEFE 338

Matches

Conservative

36;

Indels

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Gaps

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Query Match
Best Local S
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CHARACTERIZATION, AND VARIANT UBIE401.
MEDLINE-97197541; PubMed-9045837;
Lee P.T., Hsu A.Y., Ha H.T., Clarke C.F.;
The P.T., Hsu A.Y., Ha H.T., Clarke C.F.;
A C-methyltransferase involved in both ubiquinone and identification of the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from 84.
Science
[2]
                                                                       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 179:1748-1754(1997).

-!- FUNCTION: CONVERTS DDMQH2 INTO DMQH2 AND DMKH2 INTO MKH2.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 2-POLYPRENYL-6-METHOXY-1,4-BENZOQUINOL - S-ADENOSYL-L-HOMOCYSTEINE + 2-POLYPRENYL-3-METHYL-6-METHOXY-1,4-BENZOQUINOL.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DEMETHYLMENAQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12 / MG155;
STRAIN-K12 / MG155;
MEDLINE-92358234; PubMed=1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coll genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992
15-JUL-1998
15-JUL-1999
                                                                                                                                                 pfam; pF01209; Ubie_methyltran;
pROSITE; pS01183; UBIE_1; 1.
pROSITE; pS01184; UBIE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis: isolation and
ubiE gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
                                                                                                                   Menaquinone biosyn
Methyltransferase.
                                                                                                                                                                                                EcoGene; EG11473; ubiE. InterPro; IPR000339; -.
                                                                                                                                                                                                                                          EMBL; M87049; AAA67628.1; EMBL; AE000459; AAC76836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBIQUINONE/MENAQUINONE (EC 2.1.1.-).
                                                                                                       VARIANT
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                                                                                                                                                                                                                            PIR; S30722; S30722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B.,
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               Similarity
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                                                                                                                                   biosynthesis;
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Last annotation update)
E BIOSYNTHESIS METHYLTRANSFERASE UBIE
                                                                          WW;
                                                                                                                                    Ubiquinone biosynthesis; Transferase;
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Score 144; DB Pred. No. 0.00 % Mismatches
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-> L (IN REF. 1).
646F3E09A0075A9E
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL 37.1 KDA PROTEIN IN TRANSPOSON TN4556.
Streptomyces fradiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siemieniak D.R., Slightom J.L., Chung S.T.;
"Nucleotide sequence of Streptomyces fradiae transposable
Tn4556; a class-II transposon related to Tn3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSPOSON-Tn4556;
MEDLINE-90185236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRFR
                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transferase; Methyltransferase; Transposable element.
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                                                                       390
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                                                                                                   LGDIHTLPLEDGSIDCARTDRVLQHVADPAQALAEARRVLRPGGRLVMGEPDWDSLTIDY
                                                                                                                               VADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVLIS---
                                                                                                                                                             LDARPGESALDLGCGPGTDLGTLAKAVSPSGRVIGIDSSQEMVEQARRRTENLP-AVEVE
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                                                                                                                                                                                                                                                                                                                                         Pro; IPR000339; -.
PF01209; Ubie_methyltran; 1.
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nilarity . 26.9%;
Conservative 2
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                                        PDLEVS----RAYTRHVTDKIVRNGVIGRQLARLALDAGF
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RESULT

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RESULT 9
GRCB_LACLA
ID GRCB_L
AC P49016
DT 01-FEB
DT 01-FEB
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086169;
30-MAY-2000
30-MAY-2000
30-MAY-2000
  GRCB_LACLA
P49016;
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a novel gene cluster participating in menaquinone (vitamin K2) biosynthesis. Cloning and sequence determination of the 2-heptaprenyl-1,4-naphthoquinone methyltransferase gene of Bacillus stearcthermophilus.";

J. Biol. Chem. 272:12380-12383(1997).

-i- FUNCTION: CONVERTS DMKH2 INTO MKH2.

-i- CATALYTIC ACTIVITY: S-ADENOSYL-1-METHIONINE + DEMETHYLMENAQUINOL-S-ADENOSYL-1-HOMOCYSTEINE + MENAQUINOL.

-i- PATHWAY: LAST STEP IN MENAQUINONE BIOSYNTHESIS.

-i- SIMILARITY: BELONGS TO THE UBIE FAMILY.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2-HEPTAPRENTL-1,4-NAPHTHOQUINONE METHYLTRANSFERASE
(MENAQUINONE BIOSYNTHESIS METHYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01183; UBIE_1; 1
PROSITE; PS01184; UBIE_2; FALSE_NEG.
Menaquinone biosynthesis; Transferas
SEQUENCE 234 AA; 27128 MW; 8C1CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000339;
Pfam; PF01209; Ubie_m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koike-Takeshita A., koyama T., Ogura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus,
Bacillus/Staphylococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus stearothermophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAHYDRMNSVISFRR------HLKWRKDVMRRMNVQKGKKALDVCCGTADWTIALA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSQY-KFNSILRYERVFGPGYVSTGGLETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMA 304
                                                                                                                                                                                                                                         AKSYEEYSWLQESAREFPGRDELAEMFRAAGFVDV
                                                                                                                                                                                                                                                                                         --SAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 47; Conserv
     (Rel.
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                                                                                         STANDARD;
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Last sequence
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Pred. No. 0.0057
2; Mismatches
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InterPro; IPR000339; -.
Pfom; PF01209; Ubie_methyltran; 1
PROSITE; PS01183; UBIE_1; 1.
PROSITE; PS01184; UBIE_2; 1.
PROSITE; PS01184; UBIE_2; 1.
                           UBIG_ECOLI STANDARD; PRT; 240 AA.
P17993; P76924;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.
                                                                                                                _ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93374846; PubMed-8366036;
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                                                                                                                                                                                                       428
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            ,4-DIHYDROXY-5-HEXAPRENYLBENZOATE METHYLTRANSFERASE) (DHHB
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                                                                                                                                                                                                                                                                                                                                                                                                                                      YVKS--KKNONOISWLWOKVDSEDDKGFORFLDSSOYKFNSILRYERVFGPGYVSTGGLE 272
                                                                                                                                                                                                                                  SHPTLPIYKQAFELYFKNVMPFLGKVFAKSLKEYQWLQKSAEDFPDAKTLEELFRKAGFV
                                                                                                                                                                                                                                                                                           EAKKNIEFLQGNAMALPFEKGSFDVVTIGYGLRNTPDYLTVLKEIFRVLKPGGRVVCIET
                                                                                                                                                                                                                                                                                                            GLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDKPALFRSFHKWLKPGGKVL----
                                                                                                                                                                                                                                                                                                                                                                              TTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENY--DVEVVGIDLSINMISFALER-SI 329
                                                                                                                                                                                                                                                                                                                                                                                                           YNKSMTKVNEERVQEIFNSISSDYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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MW; 7D971E3A4BD804ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 134.5;
Pred. No. 0.00
14; Mismatches
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97;
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Streptococcaceae;
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                               .64)
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EMBL; Y00544; CAA68610.1; -. EMBL; M87509; AAA24714.1; -. EMBL; AE000313; AAC75292.1; -. EMBL; D90854; BAA16049.1; -. EMBL; D90855; BAA16051.1; -. PIR; S03757; S03757. PIR; S47682; A47682.
                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12 / MG1655; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITINE—3123968; PubMed=1479344;
MEDITINE—31123968; PubMed=1479344;
Wu G., Williams H.D., Zamanian M., Gibson F., Poole R.K.;
"Isolation and characterization of Escherichida coli mutants affected in aerobic respiration: the cloning and nucleotide sequence of ubiG. Identification of an S-adenosylmethionine-binding motif in protein, RNA, and small-molecule methyltransferases.";
J. Gen. Microbiol. 138:2101-2112(1992).
                                                                                                                                                                                                                                               the
                                             EcoGene; EG11143; ubiG.
InterPro; IPR000339; -.
                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                 Ubiquinone
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SUBUNIT: HOMODIMER (PROBABLE).
SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
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PF01209; Ubie_methyltran; 1.
inone biosynthesis; Transferase; Methyltransferase
NCE 240 AA; 26555 MW; D4EB4707A06F5613 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last annotation update)
ATP SYNTHASE SUBUNITS REGION ORF 1.
Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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Hypothetical protein
SEQUENCE 417 AA;
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-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE +
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01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-1994 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
3,4-DIHYDROXY-5-HEXAPRENYLBENZOATE METHYLTRANSFERASE)
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PIR; S32628; S32628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 GYVS--TGGLETTKEFVSKLDLKPGQKVLDVGCGIGGGDFYMAENYDVE---VVGIDLSI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-DEMETHYLUBIQUINONE-9 =
                                                                                                                                                                                                                                      KWLKPGGKVLISDYCKSA-----GTPSAEFAAYIRQRGYDLHDVKAYGKMLKDAGFVEVI 430
                                                                                                                                                                                                          QLVKPGGEVFFSTLNRNGKSWLMAVVGAEYILRMVPKG--THDVK---KFIKPAELLSWV
                                                                                                                                                                                                                                                                                                      EPLQVA--KLHALESGIEVEYVQETVEEHAAKHAQQYDVVTCMEMLEHVPDPQSVVHACA 113
                                                                                                                                                                                                                                                                                                                                                     NMISFALERSIGLKCAVEFEVADCTKKDYP---ENSFDVIYSRDTILHIQDKPALFRSFH
                                                                                                                                                                                                                                                                                                                                                                                                    GYITERSGGLF------GKKVLDVGC--GGG--ILAESMAREGATVTGLDMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X72948; CAA51451.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.9%; Score 127.5; DB 1; 26.4%; Pred. No. 0.017;
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PRT;
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212
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Best Local
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                                                                                                               P25397; P76866;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
TELLURITE RESISTANCE PROTEIN TEHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q55423;
15-JUL-1999
15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCG6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
MEDLINE-91285417; PubMed-2060788;
             STRAIN-K12
                        SEQUENCE FROM N.A
                                                   NCBI_TaxID=562;
                                                                Escherichia
                                                                             Bacteria;
                                                                                           Escherichia
                                                                                                                                                                                    TEHB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Tanaka A.,
Sugiura M., Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE METHYLTRANSFERASE SLL0829 (EC 2.1.1.-).
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                                                                                                                                                                                                                                                     190
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                                                                                                                                                                                                                                                                             VIAENRTDQFIQVLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro; IPR000339; -.
PF01209; Ubie_methyltran; 1.
hetical protein; Transferase; Methyltransferase.
hCE 212 AA; 23071 MW; BAD77E2E605A7001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                             Proteobacteria;
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                                                                                                                                                                                    STANDARD;
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27.7%;
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                                                                             gamma
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Pred. No. 0.
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                                                                             subdivision;
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                                                                             Enterobacteriaceae,
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Best Local :
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or send a
                                                                                                                                                                                                 EcoGene; EG11884; tehB.
Antibiotic resistance;
SEQUENCE 197 AA; 225
                                                                                                                                                                                                                                                             EMBL; M74072; AAA19564.1; -.

EMBL; AE000240; AAC74512.1; -.

EMBL; D90782; BAA15059.1; -.

EMBL; D90783; BAA15064.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mo Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              within the terminus of Escherichia coli K-12.";
J. Bacteriol. 176:2740-2742(1994).
-!- FUNCTION: RESPONSIBLE FOR POTASSIUM TELLURITE RESISTANCE
                                                                                                                                                                                                                                                PIR; JQ1018; JQ1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter E.G., Weiner J.H., Taylor D.E.;
"Nucleotide sequence and overexpression of the tellurite-resistance determinant from the IncHII plasmid pHH1508a.";
Gene 101:1-7(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor D.E., Hou Y., Turner R.J., Weiner J.H., "Location of a potassium tellurite resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94222856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97251357;
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STRAIN=K12 / MG1655;
                              312
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58
                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRESENT IN HIGH COPY NUMBER, PROBABLY BY INCREASING THE REDUCTION RATE OF TELLURITE TO METALLIC TELLURIUM WITHIN THE BACTERIUM. OTHERWISE, PHENOTYPICALLY SILENT.
SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE PLASMID ENCODED.
                                                                          ILRYERVFGPGYVSTGGLETTKEFVSKLD-LKPGQKVLDVGCGIGGGDFYMAEN-YDVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
----WDKNAMSIANVERIKSIENLDNLHTRVVDLNNLTF-DRQYDFILSTVVLMFLEAKT
                         VGIDLSINMISFA-LER--SIGLKCAVEFEVADCTKKDYPENSFDVIYSRDTILHIQDK-
                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                   Similarity
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                                                                                                                                                                                                  resistance; Tellurium
197 AA; 22531 MW; BE
                                                                                                                        Conservative
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                                                                                                                                      4.8%;
28.6%;
                                                          -RTHSEVLEAVKVVKPG-KTLDLGCGNGRNSLYLAANGYDVDA
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Pred.
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BF0D2D64F9B9C2E8
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No. 0.0
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syhew G.F.,
Rose D.J.,
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., FieldS C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; Science 269:496-512(1995).
-i- SIMILARITY: WEAK, TO YEAST ERG6 AND TO OTHER METHYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN H10095.
                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transferase; Methyltransferase. SEQUENCE 251 AA; 28050 MW; 75C3891A55D485B6 CRC64;
                                                                                                                                                                                                                                                                                                                                          EMBL; U32695; AAC21772.1; -. TIGR; HI0095; -.
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MEDLINE-95350630; PubMed-7542800;
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NCBI_TaxID=727;
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                                   384 VLISD 388
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                                                                    EAN-GLQEKIHVQRANAMKLPFEDESEDIVINEAMLTMLPVEAKKKAIAEYFRVLKPNGL 140
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                                                                                                                                                                                                              4.7%; Score 123; DB 1; Length 251; 25.6%; Pred. No. 0.047; tive 30; Mismatches 57; Indels
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Search completed: September 20, 2001, 16:21:26

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Title:
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Maximum Match 100%
Listing first 45 summaries
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2598
1 MAASAMGVLQEREVFKKYWI.....KLVRTTEGEQQWGLFIAKKM 494
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	φ	ψ	4	ω	2	1	No.	Result
189	189.5	189.5	189.5	191	193.5	196	199	204.5	207	207	223	449.5	498.5	767.5	1287.5		2105.5	2598	Score	
7.3	7.3	7.3	7.3	7.4	7.4	7.5	7.7	7.9	8.0	8.0	8.6	17.3	19.2	29.5	49.6	80.6	81.0	100.0	Match Length	Query
272	387	283	275	367	279	346	278	317	363	363	565	495	437	180	374	498	491	494	ength DB	
2 052570	2 Q9PNB2	2 Q9X5Q9	2 Q9X5Q8	10 Q43445	2 Q9KJ21	10 082720	2 Q9EYI2	2 Q55809	10 Q41587	_	2 Q9KJ20	5 Q23552	5 Q22993	10 · Q9LP64	10 Q9LP63	10 Q9LVH3	10 Q9FR44	10 Q9M571)B ID	
052570 amycolatops	Q9pnb2 campylobact	Q9x5q9 streptomyce	Q9x5q8 streptomyce	Q43445 glycine max	Q9kj21 ectothiorho	082720 nicotiana t	Q9eyi2 streptomyce	Q55809 synechocyst	Q41587 triticum ae	Q41586 triticum ae	Q9kj20 actinopolys	Q23552 caenorhabdi	Q22993 caenorhabdi	Q91p64 arabidopsis	Q91p63 arabidopsis	Q91vh3 arabidopsis	Q9fr44 arabidopsis	Q9m571 spinacia ol	Description	

4 5	44	43	42	41	40	39	3 8	37	36	35	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21	20
159.5	159.5	160	160	162.5	163.5	165.5	166	169.5	171	173	174.5	175.5	175.5	176.5	177	178	179	182	182	183.5	184	184	185	187	187.5
6.1	6.1	6.2	6.2	6.3	6.3	6.4	6.4	6.5	6.6	6.7	6.7	6.8	6.8	6.8	6.8	6.9	6.9	7.0	7.0	7.1	7.1	7.1	7.1	7.2	7.2
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052025	P94922	Q9LN25	Q39227	064850	Q9X036	Q9TYP1	Q9ZKG8	Q9EZC1	025171	024328	Q9V268	082426	Q9S0N6	Q54095	Q9XIP9	Q9ZSK1	Q9RNB8	P93852	049215	Q9RSD7	Q9KZ58	082434	P74388	Q9LM02	057965
052025 halobacteri	P94922 mycobacteri	Q9ln25 arabidopsis		064850 arabidopsis	Q9x036 thermotoga	Q9typ1 caenorhabdi	Q9zkg8 helicobacte	Q9ezcl staphylococ	025171 helicobacte	O24328 ricinus com	Q9v268 pyrococcus	O82426 oryza sativ	Q9s0n6 streptomyce	Q54095 saccharopol	Q9xip9 arabidopsis	Q9zskl arabidopsis	Q9rnb8 microcystis	zea mays	049215 zea mays (m	Q9rsd7 deinococcus	Q9kz58 streptomyce	O82434 nicotiana t	P74388 synechocyst	Q91m02 arabidopsis	057965 pyrococcus

ALIGNMENTS

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61 LELGAGIGRFTGELAEKASQVIALDFIESVIKKNESINGHYKNVKFWCADVTSPSLNISP 120 		1 maasamgvlqerevekkywiehsvdltveammldsqasdldkverpevlsmlppyegksv 60	Query Match 100.0%; Score 2598; DB 10; Length 494; Best Local Similarity 100.0%; Pred. No. 1.4e-168; Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Transferase; Methyltransferase. SEQUENCE 494 AA; 56361 MW; 7F2537C8E4B8413B CRC64;	IPR001601;	InterPro; IPR000780;	InterPro; IPRO00051;	J. B101. Chem. 2/5:14095-14101(2000). FMRT. AF037633: AAF61950 1: -	the recombinant enzyme.";	complementation in Schizosaccharomyces pombe and characterization of	inach:	Nuccio M.L., Ziemak M.J., Henry S.A., Weretilnyk E.A., Hanson A.D.;	MEDLINE=20261526; PubMed=10799484;	TISSUE=SALINIZED LEAF;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=3562;	Caryophyllales; Chenopodiaceae; Spinacia.	Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	Spinacia oleracea (Spinach).	PEAMT.	$\overline{}$	(TrEMBLrel. 16,	15,	01-OCT-2000 (TremBLrel. 15, Created)		O9MS71 PRELIMINARY: PRT: 494 AA.	RESULT 1

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01-MAR-2001
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                                                                                                                                                                                  S-Adenosylmethionine:Phospho-Ethanolamine Plant Physiol. 124:1800-1813 (2000). EMBL; AF197940; AAG41121.1; -. Transferase; Methyltransferase. SEQUENCE 491 AA; 56102 MW; DA4404EBED:
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01-MAR-2001 (TIEMBLIE1. 16, Last sequence update)
01-MAR-2001 (TIEMBLIE1. 16, Last annotation update)
sam:PHOSPHO-ETHANOLAMINE N-METHYLTRANSFERASE.
                                                                                                                                                                                                                                      STRAIN-CV. LANDSBERG ERECTA; TISSUE-STAGE MEDILINE-20567827; PubMed-1115895; Bolognese C.P., McGraw P.; The Isolation and Characterization in Yea
                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Trache.
Magnoliophyta; eudicotyledons; core eudicots;
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MAASAMGVLQEREVFKKYWIEHSVDLTVEAMMLDSQASDLDKVERPEVLSMLPPYEGKSV
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78
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01-MAR-2001 (TrEMBLrel. 16, Last annotation up
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A Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hop A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Akhan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., A Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., A Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., A Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspie A Theologis A., Ecker J.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AC020889; AAF79705.1; -.

R InterPro; IPR001601; -.
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Q9LP63;
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Best Local Similarity
Matches 243; Conser
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Q9LP64;
Q1-OCT-2000
01-OCT-2000
01-MAR-2001
T1N15.22;
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., K
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., K
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thave
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.
Boker J.R.;
 Cheuk R.,
Khan S., K
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidomai
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                                    SEQUENCE FROM N.A.
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36; Mismatches
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J., Choi E.,
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                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
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Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Fed
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC020889; AAF79704.1; -.
InterPro; IPR000780; ...
InterPro; IPR000780; ...
                                                                     STRAIN-BRISTOL N2;
Pauley A., Gattung
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               STRAIN-BRISTOL N2;
                              SEQUENCE FROM N
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                           Nature 368:32-38(1994).
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Lenz C., Li
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Pham P., Sa
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75.4%;
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01, Last sequence up
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                                                        the EMBL/GenBank/DDBJ databases
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A., Liu J., Liu S., Mukharsky N.,
Sakano H., Schwartz J., Southwick A.,
berg M., Yu G., Davis R., Federspiel P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 7e-1
9; Mismatches
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Best Loc
Matches
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Q23552;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2000
elegans.
Nature 3
[2]
                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M. Gentiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
CODED FOR BY C. ELEGANS CDNA YK92B11.3.
                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE~94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                        Eukaryota; M
Rhabditidae;
                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Methyltransferase SEQUENCE 437 AA; 49769 MW;
                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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127; Conserv
                  368:32-38(1994)
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                                                                                                                                                                                                                                                                        Peloderinae;
                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; rinae; Caenorhabditis.
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Pred. No. 4.6e-26;
0; Mismatches 156;
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                                                                                                                                                    Johnston L.,
                                                                                                                                                                                                                                                                                        Rhabditoidea;
                                                                                                         Shownkeen
                                                                                                                                                                                Coulson
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EMBL; U39998; AAA81102:1;
InterPro; IPR000051; -.
InterPro; IPR001601; -.
SEQUENCE 495 AA; 57262
       MEDLINE-20357342; PubMed-10896553;
Nyyssola A., Kerovuo J., Kaukinen P., v
"Extreme halophiles synthesize betaine
J Biol. Chem. 275:22196-22201(2000).
EMBL; AF216583; AAF87204.1; -.
InterPro; IPR000551; -.
InterPro; IPR001601; -.
                                                                                                                                                                                 O9KJ20:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLYCINE-SARCOSINE-DIMETHYLGLYCINE METHYLTRANSFERASE
                                                                                                                    Actinopolyspora.
NCBI_TaxID=1850;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                               Actinomycetales; Pseudonocardineae;
                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                      Actinopolyspora halophila
                                                                                                                                                                                                                                                 Q9KJ20
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[3]
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137; Conserv
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                                                                                                                                                                                                                                                 PRELIMINARY;
Methyltransferase
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Pred. No. 1.2e-22;
4; Mismatches 195
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01-NOV-1996
01-FEB-1997
01-JUN-2000
                                                                                                Subramaniam K., Ueng P.P.;
Submitted (JUN-1996) to the EMBL
EMBL; U60754; AAB37769.1; -
Mendel; 10873; Triae;1138;10873.
                                                                                                                                                                                                     Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-TUN-2000 (TrEMBLrel. 14, Last annotation updat
DELTA-24-STEROL METHYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                        Q41586
                                                              Transferase; SEQUENCE 3
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                                                                                        InterPro; IPR000051;
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  68;
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  Conservative
                                                             Methyltransferase.
63 AA; 41603 MW;
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; Poales; Poaceae; Pooideae; Triticeae;
  38;
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Score 207; DB
Pred. No. 2.2e
38; Mismatches
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Pred. No. 3
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             DB 10;
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Q55809;
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-MAR-2001 (TrEMBLrel.)
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01-JAN-1998
01-JUN-2000
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Subramaniam K., Ueng P.P.;
Submitted (JUN-1996) to the EMBL
EMBL; U60755; AAB49338.1; -
Mendel; 10874; Triae;1138;10874.
                        DELTA(24)-STEROL C-METHYLTRANSFERASE ERG6 OR SLR0089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000051; -.
Transferase; Methyltransferase.
SEQUENCE 363 AA; 41636 MW; 7F20995861A62C75
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Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
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Best Local :
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Q9EYI2;
01-MAR-2001
01-MAR-2001
01-MAR-2001
"The entire nogalamycin bios nogalater; Characterization hybrid structures."; Submitted (NOV-2000) to the
                                                                                                                                                                                                                                   Streptomyces nogalater.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061201; Pudmeu-oyuzuz,
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nak
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
                                                                                                                                                                                                                                                                                                          SNOGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cya
Synechocystis sp. strain PCC6803. I. Sequence features
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                           STRAIN-ATCC27451;
                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                            Ylihonko K.;
                                                                                                                     rorkkell
                                                                                                                                                                                                             NCBI_TaxID=38314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:109-136(1996).
EMBL; D64004; BAA10562.1; -.
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Kaneko T., Tanaka A., Sato S., Kotani H.,
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NCBI_TaxID=1148;
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                                                                                                                     Kunnari
                                                                                                                  Τ.,
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tion of a 20 1
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                                                                                                                     Palmu
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  EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No. 2.7e-06;
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                                                                                                                     Mantsala
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Best Local S
Matches 62
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Best Local S
Matches 55
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Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core euc
Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
S-ADENOSYL-METHIONINE-STEROL-C- METHYLTRANSFERASE.
 Q9KJ21
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                                                                                  215
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mes 62; Conserv
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                                                                                NNEEHNRIKAEIELGNGLPEVRLTTQCLEAAKQAGF-EVV
                                                                                                                                                 VKGDFMKMPFPDNSFDAVYAIEATCHAPDPLGCYKEIYRVLKPGQCFAVYEWCMTDSYNP
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NCE 278 AA;
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55; Conserved
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                                                                                                                                                                                                                                                                                               7.5%;
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Pred. No. 5.2e
48; Mismatches
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                                                                                                                                                                                                                                                                                               Score 196; DB 10;
Pred. No. 1.1e-05;
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 PRT;
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eudicots; Asteridae;
                                                                                                               KDAGFVEVI 430
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01-NOV-1996
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
SARCOSINE-DIMETHYLGLYCINE METHYLTRANSFERASE.
                                                                                                       STRAIN=CV. WILLIAMS 82; TISSUE-ETIOLATED HYPOCOTYLS; MEDILINE=96199190; PubMed=8621604; Strain J., Gonzales R.A., Bhattacharyya M.K.; "Identification and characterization of an S-adenosyl-L-methionine: delta 24-sterol-C-methyltransferase cDNA from soybean."; J. Biol. Chem. 271:9384-9389(1996).
                                                                                                                                                                                                                                                                                                                                                    Glycine max (Soybean).
Eukaryota; Viridiplantae;
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01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-UN-2000 (TIEMBLIEL. 14, Last annotation update)
S-ADENOSYL-L-METHIONINE: DELTA24-STEROL-C- METHYLTRANSFERASE
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"Extreme halophiles synthesize betaine
J. Biol. Chem. 275:22196-22201(2000).
EMBL. AF216282; AAF87203.1; -.
InterPro; IPR000051; -.
                    STRAIN=CV. WILLIAMS Clouse J.A.;
                                                                                                                                                                                                                                                                                                        Magnoliophyta; eudicotyledons; core Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20357342; PubMed=10896953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ectothiorhodospira halochloris
                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGLFIAKK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITFEDHTHQLPRHYGRVRRELDRREGELQGHVSAEYIERMKNGLDHW---VNGGNKGYLT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIAENRTDQFIQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPMQADDCPEGVIQPILDRIHLETMGTPN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVERMSSLSRQLGPDSYVLDMGAGYGGSARYLAHKYGCKVAALNLSER--ENERDRQMNK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKEFVSKL--DLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFALERSIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conservative
(DEC-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
                                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VLQKELDALEQEKDDFIDDFSEEDYNDIVDGWKAKLVRTTEGEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4%;
ç
the
                                           TISSUE=ETIOLATED HYPOCOTYLS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision;
                                                                                                                                                                                                                                                                                                                               Embryophyta; Tracheophyta; Spermatophyta;
dons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 193.5;
Pred. No. 1.2e
43; Mismatches
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579337A6915E66D5
                                                                                                                                                                                                                                                                                                            Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2e-05;
ches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weymarn N., Reinikainen T.; om glycine by methylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ectothiorhodospiraceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U43683; AAB04057.1; -.
Mendel; 8195; Glyma;1138;8195.
InterPro; IPR000051; -.
Transferase; Methyltransferase.
SEQUENCE 367 AA; 41518 MW; B3EBF8D2F0B22FB4 CRC64;
                                                                                                                                                                                                                                                                           114 PLQLGLKPGQKVLDVGCGIGGPLREISRESSTSITGLNNNEYQITRGKELNRIAGVDKTC 173
                                                                                                                                                 435 -----TDQFIQVLQKELDALEQEKDDFIDDFSEEDYNDIVDGWKAKL 476
                                                                                                                                                                                                                  395 ---TPSAEFAAYIRQRGYDLHDVKAYGK----MLKDAGFVEVIAENR------ 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 KSKKNQNQISWLWQKVDSEDDKGFQRF------LDSSQYKFNSILRYERVFGPG 264
                                                                                                       293 KSHFSLSSFRLTAVGRLFTKNMVKVL--EYVGLAPKGSLRVQDFLEKAAEGLVEGGKREI 350
                                                                                                                                                                                            234 DPQNPEHQKIKAEIEIGDGLPDIRLTAKCLEALKQAGF-EVIWEKDLAVDSPLPWYLPLD 292
                                                                                                                                                                                                                                                                                                                                                                                                        281 ---LDLKPGQKVLDVGCGIGGGDFYMAENYDVEVVGIDLSINMISFA--LERSIGLKCAV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 YVSTGGLETTK-----EFVSK------ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 HVCYGGQEEERKANYTDMVNKYYDLVTSFYEFGWGESFHFAPRWKGESLRESIKRHEHFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KKKKNRNEV----VLCSAEGTGGCSKLAAMDLASNLGGKIDKAEV-LSAVQKYEKY---- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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